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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:27:13 ; Search time 146.743 Seconds
(without alignments)
304.667 Million cell updates/sec

Title: US-10-769-144-8

Perfect score: 557

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CQQNSYPRTFGQGTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- Published Applications AA Main:
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	100.0	107	3	US-09-851-614-2
2	557	100.0	107	4	US-10-035-637-2
3	557	100.0	107	5	US-10-769-144-8
4	557	100.0	107	5	US-10-903-191-8
5	557	100.0	233	5	US-10-769-144-6
6	557	100.0	233	5	US-10-903-191-6
7	557	100.0	411	5	US-10-769-144-12
8	557	100.0	411	5	US-10-903-191-12
9	538	96.6	107	6	US-09-948-939-13
10	538	96.6	107	6	US-11-040-846-13
11	538	96.6	108	4	US-10-408-901-20
12	538	96.6	214	4	US-10-408-901-44
13	537	96.4	107	5	US-10-891-658-88
14	535	96.1	107	4	US-10-703-714-4
15	535	96.1	107	4	US-10-703-714-8
16	535	96.1	107	4	US-10-703-714-16
17	535	96.1	236	5	US-10-858-186-20
18	531	95.3	107	5	US-10-815-449-6
19	531	95.3	107	6	US-11-009-731-91
20	531	95.3	107	6	US-11-102-403-13
21	530	95.2	107	4	US-10-221-529-4
22	529	95.0	107	5	US-10-815-449-2
23	529	95.0	107	5	US-10-815-449-4
24	529	95.0	108	3	US-09-920-262A-8
25	529	95.0	108	3	US-10-912-994-8
26	529	95.0	108	5	US-10-975-883-8
27	529	95.0	108	5	US-10-975-740A-8

28	529	95.0	108	5	US-10-975-708-8	Sequence 8, Appli
29	526	94.4	107	6	US-11-102-403-5	Sequence 5, Appli
30	526	94.4	107	6	US-11-102-403-7	Sequence 7, Appli
31	524	94.1	108	4	US-10-408-901-12	Sequence 12, Appli
32	524	94.1	214	4	US-10-408-901-36	Sequence 36, Appli
33	522	93.7	107	6	US-11-102-403-15	Sequence 15, Appli
34	521	93.5	128	4	US-10-389-221-12	Sequence 12, Appli
35	521	93.5	128	5	US-10-909-851-26	Sequence 26, Appli
36	519	93.2	107	4	US-10-338-366-12	Sequence 12, Appli
37	508	91.2	107	5	US-10-727-155-312	Sequence 312, App
38	508	91.2	129	5	US-10-910-901-20	Sequence 20, Appli
39	506	90.8	107	4	US-10-041-860-43	Sequence 43, Appli
40	506	90.8	107	4	US-10-041-860-218	Sequence 218, App
41	506	90.8	107	4	US-10-685-383-64	Sequence 64, Appli
42	505	90.7	127	4	US-10-395-894-25	Sequence 25, Appli
43	505	90.7	127	4	US-10-695-667-25	Sequence 25, Appli
44	505	90.7	127	5	US-10-976-352-25	Sequence 25, Appli
45	504	90.5	107	5	US-10-727-155-122	Sequence 122, App

ALIGNMENTS

RESULT 1

US-09-851-614-2
; Sequence 2, Application US/09851614
; Publication No. US20030167502A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; FILE REFERENCE: MXI-166
; CURRENT APPLICATION NUMBER: US/09/851.614
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USN 60/203.126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USN 60/230.739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-851-614-2

Query Match	100.0%;	Score 557;	DB 3;	Length 107;
Best Local Similarity	100.0%;	Pred. No. 2.6e-42;		
Matches 107;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	DIQMTQSPSSLSASVGRVTITCRASQGISRWLA	YQOKPEKAPKSLIYAASSLSQGVPS	60
Db	1	DIQMTQSPSSLSASVGRVTITCRASQGISRWLA	YQOKPEKAPKSLIYAASSLSQGVPS	60
Qy	61	RFSGSGSGTDFTLTISGLQPEDFATYYCQVNSYPRTFGQGTKVEIK	107	
Db	61	RFSGSGSGTDFTLTISGLQPEDFATYYCQVNSYPRTFGQGTKVEIK	107	

RESULT 2

US-10-035-637-2
; Sequence 2, Application US/10035637
; Publication No. US20030031667A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035.637
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/851.614

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; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USSN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-035-637-2

Query Match      100.0%; Score 557; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

Qy 61 RFSGSGGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGQTKVEIK 107
Db 61 RFSGSGGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGQTKVEIK 107

RESULT 3
US-10-769-144-8
; Sequence 8, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10769,144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-8

Query Match      100.0%; Score 557; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

Qy 61 RFSGSGGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGQTKVEIK 107
Db 61 RFSGSGGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGQTKVEIK 107

RESULT 4
US-10-903-191-8
; Sequence 8, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
```

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; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-8

Query Match      100.0%; Score 557; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

Qy 61 RFSGSGGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGQTKVEIK 107
Db 61 RFSGSGGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGQTKVEIK 107

RESULT 5
US-10-769-144-6
; Sequence 6, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-6

Query Match      100.0%; Score 557; DB 5; Length 233;
Best Local Similarity 100.0%; Pred. No. 5.6e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 20 DIQWTQSPSSLSASVGDVRTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 79

Qy 61 RFSGSGGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGQTKVEIK 107
Db 80 RFSGSGGTDFTLTISGLQPEDFATYCCQYNSYPRTFGGQTKVEIK 126

RESULT 6
US-10-903-191-6
; Sequence 6, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
```


Db 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPTFFGGTKVEIK 107

RESULT 10

US-10-408-846-13
; Sequence 13, Application US/11040846
; Publication No. US20050201994A1
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
; APPLICANT: Halk, Edward L.
; APPLICANT: Lonberg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/11/040,846
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/948,939
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 09/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: light chain variable region predicted sequence for
; OTHER INFORMATION: 1E2 from V κ L-15
US-10-408-846-13

Query Match 96.6%; Score 538; DB 6; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.3e-40;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPTFFGGTKVEIK 107

Db 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPTFFGGTKVEIK 107

RESULT 11

US-10-408-901-20
; Sequence 20, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-20

Query Match 96.6%; Score 538; DB 4; Length 108;
Best Local Similarity 97.2%; Pred. No. 1.3e-40;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPTFFGGTKVEIK 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPTFFGGTKVEIK 107

RESULT 12

US-10-408-901-44
; Sequence 44, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-44

Query Match 96.6%; Score 538; DB 4; Length 214;
Best Local Similarity 97.2%; Pred. No. 2.6e-40;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPTFFGGTKVEIK 107

Db 61 RFGSGSGTDFTLTISLQPEDFATYYCQYNSYPTFFGGTKVEIK 107

RESULT 13

US-10-891-658-88
; Sequence 88, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-88

Search completed: December 3, 2005, 14:17:34
Job time : 147.743 secs

Query Match 96.1%; Score 535; DB 4; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.4e-40;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Db 197 RFSGSGGTDTLTITSLQPEDFATYYCQANSPLTFGGTKVEIK 243

RESULT 2

US-11-144-248-52
; Sequence 52, Application US/11144248
; Publication No. US20050244408A1

GENERAL INFORMATION:

; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-144-248-52

Query Match 87.3%; Score 486; DB 7; Length 236;

Best Local Similarity 89.7%; Pred. No. 8.2e-32; Mismatches 2; Indels 0; Gaps 0;
Matches 96; Conservative 2;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQSGVPS 60

Db 23 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQSGVPS 82

Qy 61 RFSGSGGTDTLTITSLQPEDFATYYCQVNSYPRTFGGTKVEIK 107

Db 83 RFSGSGGTDTLTITSLQPEDFATYYCLOHNSYPTWTFGGTKVEIK 129

RESULT 3

US-11-084-554-126
; Sequence 126, Application US/11084554
; Publication No. US20050260679A1

GENERAL INFORMATION:

; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-084-554-126

Query Match 86.9%; Score 484; DB 7; Length 95;

Best Local Similarity 97.9%; Pred. No. 5.5e-32; Mismatches 0; Indels 0; Gaps 0;
Matches 93; Conservative 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQSGVPS 60

Qy 61 RFSGSGGTDTLTITSLQPEDFATYYCQVNSYPRTFGGTKVEIK 95

Db 61 RFSGSGGTDTLTITSLQPEDFATYYCQVNSYPRTFGGTKVEIK 95

RESULT 4

US-11-084-554-1
; Sequence 1, Application US/11084554
; Publication No. US20050260679A1

GENERAL INFORMATION:

; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-084-554-1

Query Match 86.9%; Score 484; DB 7; Length 107;

Best Local Similarity 88.8%; Pred. No. 6e-32; Mismatches 3; Indels 0; Gaps 0;
Matches 95; Conservative 3;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQSGVPS 60

Qy 61 RFSGSGGTDTLTITSLQPEDFATYYCQVNSYPRTFGGTKVEIK 107

Db 61 RFSGSGGTDTLTITSLQPEDFATYYCQVNSYPRTFGGTKVEIK 107

RESULT 5

US-11-144-248-48
; Sequence 48, Application US/11144248
; Publication No. US20050244408A1

GENERAL INFORMATION:

; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-144-248-48

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; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 261
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-261

Query Match      86.7%; Score 483; DB 7; Length 244;
Best Local Similarity 87.9%; Pred. No. 1.4e-31;
Matches 94; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSIQLSGVPS 60
      |||
Db      137 DIQMTQSPSSLSASIGDRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSIQLSGVPS 196

QY      61 RFSGSGSGTDFTLTISGLQPEDPATYCYCOQYNSYPRTFGQGTKEIK 107
      |||
Db      197 RFSGSGSGTDFTLTISGLQPEDVATYCYCKYNSAPYAFGQGTKEIK 243

RESULT 8
US-11-054-669-62
; Sequence 62, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-62

Query Match      86.0%; Score 479; DB 7; Length 95;
Best Local Similarity 96.8%; Pred. No. 1.3e-31;
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSIQLSGVPS 60
      |||
Db      1 DIQMTQSPSSLSASVGRVTITCRAGISSWLAWYQOKPEKAPKSLIYAASSIQLSGVPS 60

QY      61 RFSGSGSGTDFTLTISGLQPEDPATYCYCOQYNSYP 95

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```
Db 61 RFSGSGSGTDTLTITISLQPEDFATYCCQYNSYP 95
|||||
Query Match 86.0%; Score 479; DB 7; Length 113;
Best Local Similarity 86.7%; Pred. No. 1.5e-31;
Matches 98; Conservative 2; Mismatches 7; Indels 6; Gaps 2;

RESULT 9
US-11-096-074-53
; Sequence 53, Application US/11096074
; Publication No. US2005026193A1
; GENERAL INFORMATION:
; APPLICANT: LIEBERBURG, IVAN
; TITLE OF INVENTION: STEROID SPARING AGENTS AND METHODS OF USING SAME
; FILE REFERENCE: 034008-112
; CURRENT APPLICATION NUMBER: US/11/096,074
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/558,120
; PRIOR FILING DATE: 2004-04-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 53
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (31)..(32)
; OTHER INFORMATION: Variable amino acid
US-11-096-074-53

Query Match 86.0%; Score 479; DB 7; Length 113;
Best Local Similarity 86.7%; Pred. No. 1.5e-31;
Matches 98; Conservative 2; Mismatches 7; Indels 6; Gaps 2;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQ-----GISRLAWYQOKPEKAPKSLIYAASLIQ 55
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSLVXXISNYLAWYQOKPEKAPKSLIYAASLS 60
Qy 56 SGVSRFSGSGSGTDTLTITISLQPEDFATYCCQYNSYPR-TFGQGTKEIK 107
Db 61 SGVSRFSGSGSGTDTLTITISLQPEDFATYCCQYNSLPETWTGQGTKEIK 113

RESULT 10
US-11-054-515-164
; Sequence 164, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 280
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-280

Query Match 85.8%; Score 478; DB 7; Length 244;
Best Local Similarity 86.9%; Pred. No. 3.5e-31;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRLAWYQOKPEKAPKSLIYAASLIQSGVPS 60
Db 137 DIQMTQSPSSLSASIGDRVTITCRASQIRNYLAWYQOKPEKAPKSLIYAASLIQSGVPS 196
Qy 61 RFSGSGSGTDTLTITISLQPEDFATYCCQYNSYPRTFGQGTKEIK 107
Db 197 RFSGSGSGTDTLTITISLQPEDVAAYYQKYNAPYAFGQGTKEIK 243

RESULT 11
US-11-054-515-280
; Sequence 280, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 280
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-280

Query Match 85.8%; Score 478; DB 7; Length 244;
Best Local Similarity 86.9%; Pred. No. 3.5e-31;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRLAWYQOKPEKAPKSLIYAASLIQSGVPS 60
Db 137 DIQMTQSPSSLSASIGDRVTITCRASQIRNYLAWYQOKPEKAPKSLIYAASLIQSGVPS 196
Qy 61 RFSGSGSGTDTLTITISLQPEDFATYCCQYNSYPRTFGQGTKEIK 107
Db 197 RFSGSGSGTDTLTITISLQPEDVAAYYQKYNAPYAFGQGTKEIK 243

RESULT 12
US-11-054-515-1882
; Sequence 1882, Application US/11054515
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; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1882
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1882

Query Match      85.6%; Score 477; DB 7; Length 239;
Best Local Similarity 84.1%; Pred. No. 4.1e-31;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 132 DIQMTQSPSTLSASIGDRVTITCRASEGIYHWLAWYQOKPGKAPKLLIYKASSLSGAPS 191
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RFSGSGSGTDFTLTISGLQPEDFATYYCQYNYSYPRTFGGTKVEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 192 RFSGSGSGTDFTLTISGLQPEDFATYYCQYNYSYPRTFGGTKVEIK 238
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
US-11-054-515-1889
; Sequence 1889, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1889
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1889

Query Match      85.6%; Score 477; DB 7; Length 241;
Best Local Similarity 84.1%; Pred. No. 4.1e-31;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 134 DIQMTQSPSTLSASIGDRVTITCRASEGIYHWLAWYQOKPGKAPKLLIYKASSLSGAPS 193
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RFSGSGSGTDFTLTISGLQPEDFATYYCQYNYSYPRTFGGTKVEIK 107
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Db 194 RFGSGSGTDTLTITSSIQDDPATYCCQYSNYPLTFGGTKLEIK 240

RESULT 15

US-11-054-515-1901
 ; Sequence 1901, Application US/11054515
 ; Publication No. US20050255532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P3
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543,296
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/580,347
 ; PRIOR FILING DATE: 2004-06-18
 ; PRIOR APPLICATION NUMBER: 10/293,418
 ; PRIOR FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 1901
 ; LENGTH: 241
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-054-515-1901

Query Match 85.6%; Score 477; DB 7; Length 241;
 Best Local Similarity 84.1%; Pred. No. 4.1e-31;
 Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLQSGVPS 60
 Db 134 DIQMTQSPSTLSASIGDRVTITCRASEGIYHMLAWYQOKPGKAPKLLIYKASSLSAGAPS 193
 Qy 61 RFGSGSGTDTLTITISGLQDDPATYCCQYSNYPLTFGGTKVEIK 107
 Db 194 RFGSGSGTDTLTITISGLQDDPATYCCQYSNYPLTFGGTKLEIK 240

Search completed: December 3, 2005, 14:17:54
 Job time : 6.11429 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:48 ; Search time 188.669 Seconds
(without alignments)
400.126 Million cell updates/sec

Title: US-10-769-144-8

Perfect score: 557

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CQQNSYPRFGQTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	508	91.2	236	Q6GMX9 HUMAN	Q6gmX9 homo sapien
2	494	88.7	108	Q9UL70 HUMAN	Q9ul70 homo sapien
3	494	88.7	236	Q6GMX8 HUMAN	Q6gmX8 homo sapien
4	492	88.3	236	Q502W4 HUMAN	Q502W4 homo sapien
5	481	86.4	236	Q723Y4 HUMAN	Q723Y4 homo sapien
6	479	86.0	117	KV11 HUMAN	P01601 homo sapien
7	477	85.6	244	Q652C8 HUMAN	Q652c8 homo sapien
8	476	85.5	108	KV1G HUMAN	P01599 homo sapien
9	474	85.1	108	KV1V HUMAN	P04430 homo sapien
10	474	85.1	240	Q652C9 HUMAN	Q652c9 homo sapien
11	472	84.7	236	Q6GMW1 HUMAN	Q6gmW1 homo sapien
12	471	84.6	236	Q6PIH7 HUMAN	Q6pih7 homo sapien
13	468	84.0	108	KV1F HUMAN	P01598 homo sapien
14	467	83.8	108	KV1L HUMAN	P01604 homo sapien
15	465	83.5	108	KV1R HUMAN	P01610 homo sapien
16	461	82.8	108	Q9UL77 HUMAN	Q9ul77 homo sapien
17	460	82.6	108	Q9UL79 HUMAN	Q9ul79 homo sapien
18	460	82.6	236	Q6PIH4 HUMAN	Q6pih4 homo sapien
19	459	82.4	108	KV1H HUMAN	P01600 homo sapien
20	457	82.1	107	KV1D HUMAN	P01596 homo sapien
21	456	81.9	108	KV1A HUMAN	P01593 homo sapien
22	456	81.9	236	Q6PIT5 HUMAN	Q6pit5 homo sapien
23	455	81.8	107	Q96SA9 HUMAN	Q96sa9 homo sapien
24	453	81.3	108	KV1S HUMAN	P01611 homo sapien
25	448	80.4	234	Q72473 HUMAN	Q72473 homo sapien
26	447	80.3	108	KV1M HUMAN	P01605 homo sapien
27	446	80.1	129	KV1W HUMAN	P04431 homo sapien
28	444	79.8	107	Q9UL81 HUMAN	Q9ul81 homo sapien
29	443	79.5	108	KV1E HUMAN	P01597 homo sapien
30	443	79.5	236	Q6GMX0 HUMAN	Q6gmX0 homo sapien
31	441	79.2	108	KV1O HUMAN	P01607 homo sapien

32	440	79.0	108	1	KV1B HUMAN	P01594 homo sapien
33	439	78.8	117	1	KV1J HUMAN	P01602 homo sapien
34	438	78.6	108	1	KV1K HUMAN	P01603 homo sapien
35	435	78.1	108	1	KV1Y HUMAN	P80362 homo sapien
36	434	77.9	234	2	Q5EPF6 HUMAN	Q5ef66 homo sapien
37	433	77.7	108	1	KV1P HUMAN	P01608 homo sapien
38	429	77.0	108	1	KV1N HUMAN	P01606 homo sapien
39	428	76.8	108	1	KV1Q HUMAN	P01609 homo sapien
40	422	75.8	108	1	KV1C HUMAN	P01595 homo sapien
41	418	75.0	189	2	Q569T7 HUMAN	Q569t7 homo sapien
42	417	74.9	129	1	KV1X HUMAN	P04432 homo sapien
43	409	73.4	112	1	KV1U HUMAN	P01613 homo sapien
44	407	73.1	108	1	KV5J MOUSE	P01643 mus musculus
45	402	72.2	116	2	Q96PF6 HUMAN	Q96pf6 homo sapien

ALIGNMENTS

RESULT 1

ID Q6GMX9 HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6GMX9;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE IGKC protein.

GN Name=IGKC;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RP [1]

RN NUCLEOTIDE SEQUENCE.

RC TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Smialus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smal M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RP TISSUE=Primary B-Cells;

RC NIH MGC Project;

RG Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC073763; AAH73763.1; -, mRNA.

DR SMR; Q6GMX9; 23-236.

DR Ensembl; ENSG00000163245; Homo sapiens.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG cl.

DR InterPro; IPR003006; IG_MHC.

DR Pfam; PF07654; Cl-set; 1.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 1.

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DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;

Query Match 91.2%; Score 508; DB 2; Length 236;
Best Local Similarity 90.7%; Pred. No. 2.1e-42;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGRVTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 23 DIQWTSPPSSLSASVGRVTTTCRASQGVNVRWLAWYQORPEKAPKSLIYATSSLSHGVS 82

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQVNSYPRTFGGTKVEIK 107
Db 83 RFGSGSGTDFTLTISGLQPEDFATYYCQVNTYPLTFGGTKVEIK 129

RESULT 2
Q9UL70_HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -, mRNA.
DR SMR; Q6GMX8; 24-235.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 88.7%; Score 494; DB 2; Length 108;
Best Local Similarity 89.7%; Pred. No. 5.2e-41;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGRVTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQWTSPPSSLSASVGRVTTTCRASQGISRWLAWYQOKPKVPKSLIYAASLTLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQVNSYPRTFGGTKVEIK 107
Db 61 RFGSGSGTDFTLTISGLQPEDVATYYCQVNSAPRTFGPTKLEIK 107
```

```
RESULT 3
Q6GMX8_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -, mRNA.
DR SMR; Q6GMX8; 24-235.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR NON_TER 236 236
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 88.7%; Score 494; DB 2; Length 236;
Best Local Similarity 89.7%; Pred. No. 5.2e-41;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGRVTTTCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 23 DIQWTSPPSSLSASVGRVTTTCRASQGISRWLAWYQOKPKAPKLIYAASSLSQSGVPS 82

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQVNSYPRTFGGTKVEIK 107
Db 83 RFGSGSGTDFTLTISGLQPEDFATYYCQVNSAPRTFGPTKVDIK 129

RESULT 4
```

```
Q502W4 HUMAN
ID Q502W4 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q502W4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fafey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC095489; AAH95489.1; -; mRNA.
DR SMR; Q502W4; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG.2.
DR SMART; SM00407; IGcl.1.
DR SMART; SM00406; IGv.1.
DR PROSITE; PS00290; IG.MHC; UNKNOWN 1.
DR PROSITE; PS00290; IG.MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;

Query Match 88.3%; Score 492; DB 2; Length 236;
Best Local Similarity 89.7%; Pred. No. 8.2e-41;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISRWLAHYQOKPKAPKSLIYAASSLSQGVPS 60
DB 23 DIQMTQSPSSLSASVGDRTVITTCRASQGISRWLAHYQOKPKAPKSLIYAASSLSQGVPS 82

QY 61 RFGSGSGTDFLTITSLGQPEDFATYCYQYNSYPRTFGQGTKEIK 107
DB 83 RFGSGSGTDFLTITSLGQPEDFATYCYQYNSYPRTFGQGTKEIK 129

RESULT 5
Q7Z3Y4_HUMAN
ID Q7Z3Y4_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q7Z3Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fafey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal Muscle;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -; mRNA.
DR HSRP; P01834; 1HEZ.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00406; IGv.1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00835; IG LIKE; 2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match 86.4%; Score 481; DB 2; Length 236;
Best Local Similarity 87.9%; Pred. No. 1e-39;
Matches 94; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISRWLAHYQOKPKAPKSLIYAASSLSQGVPS 60
DB 23 DIQMTQSPSSLSASVGDRTVITTCRASQGISRWLAHYQOKPKAPKSLIYAASSLSQGVPS 82

QY 61 RFGSGSGTDFLTITSLGQPEDFATYCYQYNSYPRTFGQGTKEIK 107
DB 83 RFGSGSGTDFLTITSLGQPEDFATYCYQYNSYPRTFGQGTKEIK 129

RESULT 6
KV11_HUMAN
ID KV11_HUMAN STANDARD; PRT; 117 AA.
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
```

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10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-I region HK101 precursor (Fragment).
Homo sapiens (Human).
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Homo.
NCBI_TaxID=9606;
[1]
NUCLEOTIDE SEQUENCE.
MEDLINE=81098966; PubMed=6779204;
Bentley D.L., Rabbitts T.H.;
"Human immunoglobulin variable region genes -- DNA sequences of two V
kappa genes and a pseudogene.";
Nature 288:730-733(1980).
[2]
NUCLEOTIDE SEQUENCE.
MEDLINE=83129397; PubMed=6402305; DOI=10.1016/0092-8674(83)90508-1;
Bentley D.L., Rabbitts T.H.;
"Evolution of immunoglobulin V genes: evidence indicating that
recently duplicated human V kappa sequences have diverged by gene
conversion.";
Cell 32:181-189(1983).
-----
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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EMBL; K01322; AAA58930.1; -; Genomic DNA.
EMBL; K01324; AAA58932.1; -; Genomic DNA.
EMBL; V00558; CAA23824.1; -; Genomic DNA.
PIR; A01881; KIHUL1.
HSSP; P01607; 1BWW.
SMR; P01601; 23-116.
Ensembl; ENSG00000122156; Homo sapiens.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; P:antigen binding; NAS.
GO; GO:0006935; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG_V.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 >117 Ig kappa chain V-I region HK101.
FT REGION 23 45 Framework-1.
FT REGION 46 56 Complementarity-determining-1.
FT REGION 57 71 Framework-2.
FT REGION 72 78 Complementarity-determining-2.
FT REGION 79 110 Framework-3.
FT REGION 111 >117 Complementarity-determining-3.
FT DISULFID 45 110 By similarity.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12800 MW; D7D0PF3718CF587 CRC64;

Query Match 86.0%; Score 479; DB 1; Length 117;
Best Local Similarity 96.8%; Pred. No. 7.4e-40;
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQIGISRWLAWYQOKPKAPKSLIYAASSLSQGVPS 60
Db 23 DIQWTQSPSSLSASVGDRTVITCRASQIGISRWLAWYQOKPKAPKSLIYAASSLSQGVPS 82

Qy 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYP 95
Db 83 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYP 117

RESULT 7
Q65ZC8 HUMAN PRELIMINARY; PRT; 244 AA.
ID Q65ZC8
AC Q65ZC8
```

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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Single-chain Fv (Fragment).
Name=scFv;
Homo sapiens (Human).
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Homo.
NCBI_TaxID=9606;
[1]
NUCLEOTIDE SEQUENCE.
MEDLINE=9732799; PubMed=9219263; DOI=10.1038/nbt0797-629;
Kontermann R.B., Wing M.G., Winter G.;
"Complement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631(1997).
EMBL; Y13057; CAA73500.1; -; mRNA.
InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG_V.
SMART; SM00409; IG; 2.
SMART; SM00406; IGV; 2.
PROSITE; PS0835; IG LIKE; 2.
FT NON TER 1 1
FT NON TER 244 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 85.6%; Score 477; DB 2; Length 244;
Best Local Similarity 84.1%; Pred. No. 2.7e-39;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQIGISRWLAWYQOKPKAPKSLIYAASSLSQGVPS 60
Db 137 DIQWTQSPSSLSASVGDRTVITCRASQIGISRWLAWYQOKPKAPKSLIYAASSLSQGVPS 196

Qy 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPRTFGGTKEIK 107
Db 197 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPRTFGGTKEIK 243

RESULT 8
KVIG HUMAN STANDARD; PRT; 108 AA.
ID KVIG HUMAN STANDARD; PRT; 108 AA.
AC P01599; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
[1]
PROTEIN SEQUENCE.
MEDLINE=75059122; PubMed=4215718;
Laure C.J., Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), I. The amino acid sequence of the L-chain of
kappa-type, subgroup I.";
Hoppe-Sevler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenström's
macroglobulin.
-----
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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PIR; A01867; KIHUGL.
HSSP; P01607; 1BWW.
```

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DR SMR, P01599; 1-107.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Complementarity-determining-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Complementarity-determining-3.
FT DISULFID 23 88 Framework-4.
FT NON_TER 108 108 By similarity.
SQ SEQUENCE 108 AA; 11814 MW; CIAD3CB0F600FF73 CRC64;

Query Match 85.5%; Score 476; DB 1; Length 108;
Best Local Similarity 86.9%; Pred. No. 1.3e-39; Indels 0; Gaps 0;
Matches 93; Conservative 4; Mismatches 10;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISRWLAWSYQKPEKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISRWLAWSYQKPEKAPKSLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 107
Db 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 107

RESULT 9
KV1V HUMAN STANDARD; PRT; 108 AA.
ID Q6430;
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE "Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwalet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AU) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01878; K1HUBN.
DR HSSP; P80362; 1WTL.
DR SMR; P04430; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.

us-10-769-144-8.rup Page 5
```

```

05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
IGKC protein.
Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -, mRNA.
DR SMR; Q6GMW1; 24-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25751 MW; 5BFEGA087AFAC437 CRC64;

Query Match 84.78; Score 472; DB 2; Length 236;
Best Local Similarity 89.68; Pred. No. 8.1e-38;
Matches 95; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 IQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPSR 61
DB 24 IQMTQSPSSLSASVGRVTITCRASQGISNDLWYQOKPKAPKLLIYAASSLSQGVPSR 83

QY 62 FSGSGSGTDTFTLTISGLQPEDPATYCCQYNSYPRFTFGQGTKEIK 107
DB 84 FSGSGSGTDTFTLTISGLQPEDPATYCCQYNSYPRFTFGQGTKEIK 129

RESULT 12
Q6PIH7 HUMAN
ID Q6PIH7_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

```

```

05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
IGKC protein.
Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -, mRNA.
DR HSSP; P01607; IAR2.
DR SMR; Q6PIH7; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 84.68; Score 471; DB 2; Length 236;
Best Local Similarity 86.94; Pred. No. 1e-38;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
DB 23 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 82

QY 61 RFGSGSGTDTFTLTISGLQPEDPATYCCQYNSYPRFTFGQGTKEIK 107
DB 83 RFGSGSGTDTFTLTISGLQPEDPATYCCQYNSYPRFTFGQGTKEIK 129

RESULT 13
KVIF HUMAN
ID KVIF_HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

```

DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gortlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain."
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds."
RL Biochemistry 9:3188-3196(1970).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A90562; KIHUEU.
DR HSSP; P01607; 1BWU.
DR SMR; P01598; 1-107.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;
Query Match 84.0%; Score 468; DB 1; Length 108;
Best Local Similarity 83.2%; Pred. No. 8.4e-39;
Matches 89; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRLWYQQKPEKAPKSLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSTLSASVGDRTVITCRASQGISRLWYQQKPEKAPKSLIYAASSLSQGVPS 60
QY 61 RFGSGSGTDFLTISGLQPEDFATYYCQYNSYPRTEGQGTKEIK 107
DB 61 RFGSGSGTDFLTISGLQPEDFATYYCQYNSYPRTEGQGTKEIK 107
RESULT 14
KVIL_HUMAN
ID KVIL_HUMAN STANDARD; PRT; 108 AA.
AC P01604;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region Kue.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79237924; PubMed=112021;
RA Eulitz M., Kley H.-P., Zeitler H.-J.;
RT "The primary structure of the Bence-Jones protein Kue. The amino acid
RT sequence of the variable part of a human L-chain of the kappa-type.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC PIR; A01870; KIHUKU.
DR HSSP; P01607; 1BWU.
DR SMR; P01604; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D9084E98 CRC64;
Query Match 83.8%; Score 467; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 1.1e-38;
Matches 87; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRLWYQQKPEKAPKSLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSTQPSVGDRTVITCRASQGISRLWYQQKPEKAPKSLIYAASSLSQGVPS 60
QY 61 RFGSGSGTDFLTISGLQPEDFATYYCQYNSYPRTEGQGTKEIK 107
DB 61 RFGSGSGTDFLTISGLQPEDFATYYCQYNSYPRTEGQGTKEIK 107
RESULT 15
KVIR_HUMAN
ID KVIR_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

RP PROTEIN SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated galactose
RT in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC against 3,4-pyruvylated galactose and isolated from a patient with
CC Waldenström's macroglobulinemia.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01876; KIHUWE.
DR HSPP; P80362; 1WTL.
DR SMR; P01610; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Monoclonal antibody.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 83.5%; Score 465; DB 1; Length 108;
Best Local Similarity 84.1%; Pred. No. 1.7e-38;
Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLASVGDVRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLQSGVPS 60
Db 1 DIQWTQSPSSLASVGDVRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLQSGVPS 60
Qy 61 RFGSGSGTDTLTITISGLQPEDPATYICQYNSYPRTFGGQTKVEIK 107
Db 61 RFGSGSGTDTLTITISGLQPEDPATYICQYNSYPRTFGGQTKVEIK 107

Search completed: December 3, 2005, 14:32:20
Job time : 189.669 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:10:00 ; Search time 182.992 Seconds
(without alignments)
256.916 Million cell updates/sec

Title: US-10-769-144-8

Perfect score: 557

Sequence: 1 DIQWTQSPSSLSASVGRVT.....CQQNSYPTFGQTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	100.0	107	5	AAM48004
2	557	100.0	107	8	ADT88865
3	557	100.0	233	8	ADR46825
4	557	100.0	411	8	ADR46823
5	538	96.6	107	4	ADR46829
6	538	96.6	107	4	AAB67511
7	538	96.6	107	9	ADY70214
8	538	96.6	107	7	ADY70214
9	537	96.4	214	7	ADY70214
10	535	96.1	107	9	ADY70214
11	535	96.1	107	8	ADY70214
12	535	96.1	107	8	ADY70214
13	535	96.1	107	8	ADY70214
14	535	96.1	234	9	ADY70214
15	535	96.1	236	9	ADY70214
16	535	96.1	239	9	ADY70214
17	535	96.1	290	9	ADY70214
18	532	95.3	107	9	ADY70214
19	531	95.3	107	8	ADY70214
20	531	95.3	107	8	ADY70214
21	531	95.3	107	9	ADY70214
22	530	95.2	107	4	ADY70214
23	530	95.2	107	4	ADY70214
24	530	95.2	107	9	ADY70214

25	529	95.0	107	8	ADT88865	Adt88865 Human IGF
26	529	95.0	107	8	ADT88863	Adt88863 Human IGF
27	529	95.0	108	5	AAU76522	AAU76522 Anti-Inte
28	524	94.1	108	7	ADF11399	ADF11399 2E11 anti
29	524	94.1	214	7	ADF11423	ADF11423 2E11 anti
30	523	93.9	224	4	AAB75040	AAB75040 TRO005 Hu
31	521	93.5	128	7	ABU64274	ABU64274 Human C40
32	519	93.2	107	6	AAB38063	AAB38063 Human 5F1
33	518	93.0	224	4	AAB75044	AAB75044 TRO005 Hu
34	508	91.2	107	8	ADP22406	ADP22406 Human ant
35	508	91.2	129	7	ADZ57711	ADZ57711 Germline
36	506	90.8	107	7	ADK18619	ADK18619 Anti-huma
37	506	90.8	107	7	ADK18794	ADK18794 Anti-huma
38	506	90.8	107	8	ADL25454	ADL25454 Human mAb
39	506	90.8	124	3	RAY56723	RAY56723 Amino aci
40	505	90.7	127	6	AAE37206	AAE37206 Human AB-
41	505	90.7	127	9	AEA16227	AEA16227 Anti-huma
42	504	90.5	107	8	ADP22216	ADP22216 Human ant
43	502	90.1	108	9	AEA41087	AEA41087 Germline
44	502	90.1	127	6	AAE37204	AAE37204 Human AB-
45	502	90.1	127	9	AEA16223	AEA16223 Anti-huma

ALIGNMENTS

RESULT 1
AAM48004
ID AAM48004 standard; protein, 107 AA.
XX
AC AAM48004;
XX
DT 08-MAR-2002 (first entry)
XX
DE Human monoclonal antibody B11 variable light chain protein.
XX
KW Human; monoclonal antibody; B11; antigen binding portion; dendritic cell;
KW mannose receptor; growth; cytolysis; pathogen; virus; bacterium;
KW autoimmune disease; inflammatory disorder; rheumatoid arthritis;
KW multiple sclerosis; diabetes mellitus; immunomodulatory;
KW antiinflammatory; antirheumatic; antiarthritic; neuroprotective;
KW antidiabetic; antianemic; endocrine; dermatological; antithyroid;
KW uropathic; ophthalmological; muscular.
XX
OS Homo sapiens.
XX
FN WO200185798-A2.
XX
PD 15-NOV-2001.
XX
PF 08-MAY-2001; 2001WO-US015114.
XX
PR 08-MAY-2000; 2000US-0203126P.
XX
PA 07-SEP-2000; 2000US-0230739P.
XX
PI (MEDA-) MEDAREX INC.
XX
PI Deo YM, Keler T;
XX
DR WPI; 2002-089789/12.
XX
DR N-PSDB; ABA06023.
XX
PT New human monoclonal antibodies specific for dendritic cells, useful for
PT inhibiting growth or inducing cytolysis of a dendritic cell and treating
PT or preventing a dendritic cell mediated disease, e.g., autoimmune
disorders.
XX
PS Example 2; Fig 13; 95pp; English.
XX
CC The invention relates to human monoclonal antibodies or their antigen
CC binding portions that specifically bind to dendritic cells and has one or
CC more of the following characteristics: (a) a binding affinity constant to
CC a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability

CC to opsonise a dendritic cell; (c) the ability to internalise after
 CC binding to dendritic cells; or (d) the ability to activate dendritic
 CC cells. The isolated human monoclonal antibody or its antigen binding
 CC portion may also have any of the following characteristics: (a) mediates
 CC cytolysis of dendritic cells in the presence of human effector cells; or
 CC (b) inhibits growth of dendritic cells. The antibodies or its antigen
 CC binding portion, binds to and blocks the human mannose receptor on
 CC dendritic cells. The antibodies have immunomodulatory, antiinflammatory,
 CC antirheumatic, antiarthritic, neuroprotective, antidiabetic, antianaemic,
 CC endocrine, dermatological, antithyroid, uropathic, ophthalmological and
 CC muscular activity. The antibodies or their antigen-binding fragments are
 CC useful for inhibiting growth of a dendritic cell, inducing cytolysis of a
 CC dendritic cell, treating or preventing a dendritic cell mediated disease,
 CC detecting the presence of a dendritic cell, targeting an antigen to a
 CC dendritic cell and preventing binding of a pathogen (a virus or a
 CC bacterium) to human mannose receptor on dendritic cells. In particular,
 CC the antibodies may be used to treat, autoimmune disease, graft versus
 CC host disease, immune system or inflammatory disorders (e.g. rheumatoid
 CC arthritis), multiple sclerosis, diabetes mellitus, myasthenia gravis,
 CC pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's
 CC syndrome and Graves disease. The present sequence is that of the human
 CC monoclonal antibody B11 variable light chain, useful to the invention
 XX
 SQ Sequence 107 AA;

Query Match 100.0%; Score 557; DB 5; Length 107;
 Best Local Similarity 100.0%; Pred. No. 5e-36;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQWTQSPSSLSASVGRVITTCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60
 Db 1 DIQWTQSPSSLSASVGRVITTCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60
 Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQTKVEIK 107
 Db 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQTKVEIK 107

RESULT 2
 ADR46825
 ID ADR46825 standard; protein; 107 AA.

AC ADR46825;
 DT 18-NOV-2004 (first entry)
 XX Human antibody B11 light chain variable region protein SEQ ID NO:8.
 XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
 XX antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 XX betahCG; beta chorionic gonadotropin; antibody;
 XX T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
 XX immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
 XX CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
 XX melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
 XX antibody B11; light chain variable region.
 XX Homo sapiens.
 XX WO2004074432-A2.
 XX 02-SEP-2004.
 XX 30-JAN-2004; 2004WO-US002725.
 XX 31-JAN-2003; 2003US-0443979P.
 XX (MEDA-) MEDAREX INC.
 XX Keler T, Endres M, He L, Ramakrishna V;
 XX WPI; 2004-635555/61.
 XX N-PSDB; ADR46824.

XX New molecular conjugate having a monoclonal antibody that binds to human
 PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
 PT cytotoxic T cell response in cancers and infectious diseases.
 XX Claim 11; SEQ ID NO 8; 82pp; English.

CC The present invention describes a molecular conjugate comprising a
 CC monoclonal antibody that binds to human antigen presenting cells (APCs)
 CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
 CC comprises a heavy and/or light chain variable region derived from a human
 CC VH5-51 or VK-L15 germ-line sequence with the 98 or 95 amino acid sequences
 CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
 CC described: (1) a molecular conjugate comprising a human antibody heavy
 CC chain and a human antibody light chain, where either or both chains are
 CC linked to betahCG; (2) a molecular conjugate comprising a human single
 CC chain antibody that binds to human APCs linked to betahCG, where the
 CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
 CC (ADR46829); (3) a composition comprising any of the molecular conjugates
 CC as described above, and a carrier, optionally in combination with an
 CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
 CC against betahCG, comprising contacting any of the molecular conjugates
 CC described above with APCs such that the antigen is processed and
 CC presented to T cells in a manner which induces or enhances a T cell-
 CC mediated response against the antigen; (5) immunising a subject
 CC comprising administering any of the molecular conjugates described above,
 CC optionally in combination with an adjuvant, a cytokine which stimulates
 CC proliferation of dendritic cells and/or an immunostimulatory agent; and
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
 CC comprising forming a conjugate of the antigen and a monoclonal antibody
 CC which binds to APCs, and contacting the conjugate either in vivo or ex
 CC vivo with APCs such that the antigen is internalised, processed and
 CC presented to T cells in a manner which induces or enhances a cytotoxic T
 CC cell response against the antigen. The molecular conjugate has
 CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
 CC virucide and antimalarial activities, and can be used as a CD8 agonist,
 CC and in vaccines. The methods and compositions of the present invention
 CC are useful for inducing a cytotoxic T cell response, and in particular
 CC for treating autoimmune disorders, cancers and infectious diseases by
 CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
 CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
 CC herpes. The present sequence represents a human antibody B11 light chain
 CC variable region, which is used in the exemplification of the present
 CC invention.

XX SQ Sequence 107 AA;

Query Match 100.0%; Score 557; DB 8; Length 107;
 Best Local Similarity 100.0%; Pred. No. 5e-36;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQWTQSPSSLSASVGRVITTCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60
 Db 1 DIQWTQSPSSLSASVGRVITTCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60
 Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQTKVEIK 107
 Db 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQTKVEIK 107

RESULT 3
 ADR46823
 ID ADR46823 standard; protein; 233 AA.

XX ADR46823;
 XX 18-NOV-2004 (first entry)
 DT Human antibody B11 light chain variable region protein SEQ ID NO:6.
 XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
 XX antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 XX betahCG; beta chorionic gonadotropin; antibody;

T cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; antibody B11; light chain variable region.

Homo sapiens.

WO2004074432-A2.

02-SEP-2004.

30-JAN-2004; 2004WO-US002725.

31-JAN-2003; 2003US-0443979P.

(MEDA-) MEDAREX INC.

Keler T, Endres M, He L, Ramakrishna V;

WPI; 2004-635555/61.

N-PSDB; ADR46822.

New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.

Claim 14; SEQ ID NO 6; 82pp; English.

The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to betahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human antibody B11 light chain variable region, which is used in the exemplification of the present invention.

Sequence 233 AA;

Query Match 100.0%; Score 557; DB 8; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIQMTQSPSSLSASVSGDRVTITCRASGIGSRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Dy 20 DIQMTQSPSSLSASVSGDRVTITCRASGIGSRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 79
Oy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQQVNSYPRTFGGQTKVEIK 107
Dy 80 RFGSGSGTDFTLTISGLQPEDFATYYCQQVNSYPRTFGGQTKVEIK 126

RESULT 4

ADR46829

ID ADR46829 standard; protein; 411 AA.

XX

AC ADR46829;

XX

DT 18-NOV-2004 (first entry)

XX

DE Human pB11-betahCG molecular conjugate protein SEQ ID NO:12.

XX

KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW betahCG; beta chorionic gonadotropin; antibody;
KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW antibody B11; pB11-betahCG molecular conjugate; fusion protein.

XX Homo sapiens.

OS Synthetic.

XX

PN WO2004074432-A2.

XX

PD 02-SEP-2004.

XX

PF 30-JAN-2004; 2004WO-US002725.

XX

PR 31-JAN-2003; 2003US-0443979P.

XX

PA (MEDA-) MEDAREX INC.

XX

PI Keler T, Endres M, He L, Ramakrishna V;

XX

DR WPI; 2004-635555/61.

XX

DR N-PSDB; ADR46828.

XX

PT New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.

XX

PS Claim 16; SEQ ID NO 12; 82pp; English.

XX

CC The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to betahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and

(6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human p11-betaHCG molecular conjugate, which is used in the exemplification of the present invention.

XX Sequence 411 AA;

Query Match 100.0%; Score 557; DB 8; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.8e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQQTSPSSLSASVGDRTTTCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60
Db 20 DIQQTSPSSLSASVGDRTTTCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 79

Qy 61 RFGSGSGTDTLTISGLQPEDPATYCCQYNSYPTFGQTKVEIK 107

Db 80 RFGSGSGTDTLTISGLQPEDPATYCCQYNSYPTFGQTKVEIK 126

RESULT 5

AAB67511

ID AAB67511 standard; peptide; 107 AA.

XX AAB67511;

XX 29-MAY-2001 (first entry)

XX Light chain variable region of anti-CTLA-4 antibody 1E2.

XX Complementarity determining region; CDR; immune response; antibody;
XX cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
XX autoimmune disease; infectious disease; inflammation; allergy;
XX rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
XX multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
XX transplant rejection; graft versus host disease.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 24..34

XX /note= "CDR1"

XX Region 50..66

XX /note= "CDR2"

XX Region 89..97

XX /note= "CDR3"

XX WO200114424-A2.

XX 01-MAR-2001.

XX 24-AUG-2000; 2000WO-US023356.

XX 24-AUG-1999; 99US-0150452P.

XX (MEDA-) MEDAREX INC.

XX Korman AJ, Halk EL, Lonberg N;

XX WPI; 2001-202933/20.

XX Novel human sequence antibody that binds to human cytotoxic T lymphocyte

PT associated antigen-4, useful for inducing, augmenting or prolonging
PT immune response to antigen or for suppressing immune response in patient.
XX Claim 27; Fig 7; 127pp; English.

XX The present sequence represents the light chain variable region of human
XX antibody 1E2. This antibody specifically binds to human cytotoxic T
XX lymphocyte associated antigen-4 (CTLA-4). Such antibodies are used in
XX methods for inducing, augmenting or prolonging an immune response to an
XX antigen in a patient, where the antibodies block binding of human CTLA-4
XX to human B7 ligands. The antibodies are also useful for treating
XX autoimmune disease in a subject caused or exacerbated by increased
XX activity of T cells and for treating prostate cancer, melanoma or
XX epithelial cancer. A polyvalent or polyclonal antibody preparation
XX comprising two antibodies of the invention are useful for suppressing a
XX immune response in a patient. They are used for treating cancer,
XX infectious diseases and promoting beneficial autoimmune reactions for the
XX treatment of diseases with inflammatory or allergic components. The
XX polyvalent or polyclonal preparations are useful for treating autoimmune
XX diseases such as rheumatoid arthritis, myasthenia gravis and lupus
XX erythematosus, multiple sclerosis, insulin-dependent diabetes mellitus,
XX transplant rejection, and inflammation, graft versus host disease

XX Sequence 107 AA;

Query Match 96.6%; Score 538; DB 4; Length 107;

Best Local Similarity 97.2%; Pred. No. 1.5e-34;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQQTSPSSLSASVGDRTTTCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60

Db 1 DIQQTSPSSLSASVGDRTTTCRASQGISRWLAWYQKPKAPKSLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDTLTISGLQPEDPATYCCQYNSYPTFGQTKVEIK 107

Db 61 RFGSGSGTDTLTISGLQPEDPATYCCQYNSYPTFGQTKVEIK 107

RESULT 6

ADY70214

ID ADY70214 standard; protein; 107 AA.

XX ADY70214;

XX 02-JUN-2005 (first entry)

XX Human monoclonal antibody 5D5 VK region.

XX vaccine; antibacterial; monoclonal antibody; protective antigen;
XX lethal factor; toxin; anthrax infection; screening; detection; 5D5;
XX light chain variable region.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX Region 24..34

XX /label= CDR1

XX /note= "complementarity determining region"

XX Region 50..56

XX /label= CDR2

XX /note= "complementarity determining region"

XX Region 89..97

XX /label= CDR3

XX /note= "complementarity determining region"

XX WO2005023177-A2.

XX 17-MAR-2005.

XX 21-MAY-2004; 2004WO-US016213.

XX 21-MAY-2003; 2003US-0472636P.

PR 16-OCT-2003; 2003US-0512336P.
XX (MEDA-) MEDAREX INC.
XX Keler T, Blanset D, Vitale LA, Lowy I, Srinivasan M;
XX WPI; 2005-214725/22.
DR N-PSDB; ADY70213.
XX
XX New human monoclonal antibody that binds to Bacillus anthracis protective
PT antigen and neutralizes a Bacillus anthracis toxin, useful in preparing a
PT composition for treating or preventing anthrax infection.
XX
XX Claim 10; SEQ ID NO 18; 119pp; English.
PS
XX This invention describes a novel human monoclonal antibody which binds to
CC Bacillus anthracis protective antigen with an affinity of at least 10⁻⁷ M
CC -1 and neutralizes a Bacillus anthracis lethal factor toxin at an ED-50
CC of 5 microg/ml or less in a toxin neutralization assay. The invention
CC also describes; 1) an expression vector; 2) a transfectoma comprising the
CC expression vector; 3) a transgenic non-human animal that expresses the
CC human monoclonal antibody and that has a genome comprising a human heavy
CC chain transgene or transchromosome and a human light chain transgene or
CC transchromosome; 4) an immunoconjugate comprising the human monoclonal
CC antibody, linked to a therapeutic agent chosen from a cytotoxin or
CC radioisotope; 5) a pharmaceutical composition comprising the
CC immunoconjugate or human monoclonal antibody and a carrier or an
CC additional therapeutic agent, comprising a protective antigen vaccine or
CC a second antibody against anthrax bacteria, spores, lethal factor or
CC edema factor, Fab, F(ab')₂, Fv or single chain Fv fragment of the second
CC antibody; 6) a hybridoma that produces a detectable amount of the human
CC monoclonal antibody; 7) a method of producing the human monoclonal
CC antibody; 8) a method of inhibiting a physiological activity of Bacillus
CC anthracis protective antigen in a cell susceptible to anthrax infection;
CC 9) a method of neutralizing a Bacillus anthracis toxin in a cell
CC susceptible to anthrax infection comprising immunizing the transgenic non
CC -human animal with Bacillus anthracis protective antigen or a cell
CC expressing Bacillus anthracis protective antigen, so that antibodies are
CC produced by B cells of the animal, isolating B cells of the animal and
CC fusing the B cells with myeloma cells to form immortal hybridoma cells
CC that secrete the antibody; 10) a method of treating or preventing anthrax
CC infection in a host infected with Bacillus anthracis; 11) a method of
CC detecting the presence of Bacillus anthracis protective antigen in a
CC sample; 12) a method of treating or preventing anthrax infection in a
CC patient and 13) a method of screening for an antibody against anthrax
CC protective antigen. The human monoclonal antibody comprises human IgG1 or
CC IgG3 heavy chain variable region and a human kappa light chain variable
CC and their conservative sequence modifications. The human monoclonal
CC antibody is a Fab fragment or a single chain antibody (scFv) and is
CC produced by a hybridoma, which is prepared from a B cell obtained from a
CC transgenic non-human animal having a genome comprising a human heavy
CC chain transgene or transchromosome and a human light chain transgene or
CC transchromosome fused to an immortalized cell. The heavy or light chain
CC variable region comprises FR1, FR2, FR3, CDR2, FR3, CDR3 or FR4. The
CC heavy chain variable region having FR1, FR2, FR3 or FR4 sequences are
CC derived from the human heavy chain VH3-33 or VH3-7 germ-line sequences.
CC The light chain variable region having FR1, FR2, FR3 or FR4 sequences are
CC derived from the human light chain L15, L18 or A27 germ-line sequences.
CC The ability of the antibody to neutralize the toxin requires binding to
CC Fc receptor. This sequence represents the human monoclonal antibody 5D5
CC variable region light chain comprising a L15 V-segment and a JK4 J-
XX segment.

XX Sequence 107 AA;

Query Match 96.6%; Score 538; DB 9; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.5e-34;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

QY 61 RFSGSGSGTDFTLTISGLQPEDFATYYCQVNSYPRTFGGGTKEIK 107
DB 61 RFSGSGSGTDFTLTISGLQPEDFATYYCQVNSYPRTFGGGTKEIK 107

RESULT 7

ADF11407
ID ADF11407 standard; protein; 108 AA.

XX ADF11407;

XX 12-FEB-2004 (first entry)

XX 18B2 anti-OPGL antibody kappa chain variable region SEQ ID NO:20.

XX human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.

XX Homo sapiens.

XX WO2003086289-A2.

XX 23-OCT-2003.

XX 07-APR-2003; 2003WO-US010749.

XX 05-APR-2002; 2002US-0370407P.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;

XX WPI; 2003-845253/78.

XX N-PSDB; ADF11406.

XX New isolated antibody that specifically binds osteoprotegerin ligand,
PT useful for diagnosing or treating bone disorders, such as osteoporosis,
PT bone loss from arthritis, Paget's disease or osteopenia.

XX Claim 8; SEQ ID NO 20; 156pp; English.

XX The present invention describes an isolated human antibody (I) that
CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
CC pharmaceutical composition comprising a pharmaceutical carrier and a
CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
CC in a patient, comprising administering to a patient the pharmaceutical
CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
CC for detecting OPGL in a biological sample, comprising contacting the
CC sample with (I) under conditions that allow for binding of the antibody
CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
CC osteopathic, antiarthritic and cytostatic activities, and can be used in
CC gene therapy. The composition and methods are useful in diagnosing or
CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
CC Paget's disease or osteopenia. The antibody (I) may also be used for
CC detecting OPGL in biological samples and in identifying cells or tissues
CC that produce the protein. The present sequence represents a sequence
CC which is used in the exemplification of the present invention.

XX Sequence 108 AA;

Query Match 96.6%; Score 538; DB 7; Length 108;
Best Local Similarity 97.2%; Pred. No. 1.5e-34;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60

QY 61 RFSGSGSGTDFTLTISGLQPEDFATYYCQVNSYPRTFGGGTKEIK 107
DB 61 RFSGSGSGTDFTLTISGLQPEDFATYYCQVNSYPRTFGGGTKEIK 107

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RESULT 8
ADF11431
ID ADF11431 standard; protein; 214 AA.
XX AC ADF11431;
XX AC ADF11431;
XX DE 12-FEB-2004 (first entry)
XX DT 1882 anti-OPGL antibody light chain SEQ ID NO:44.
XX KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
XX KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
XX KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
XX OS Homo sapiens.
XX PN WO2003086289-A2.
XX PD 23-OCT-2003.
XX PF 07-APR-2003; 2003WO-US010749.
XX PR 05-APR-2002; 2002US-0370407P.
XX PA (AMGE-) AMGEN INC.
XX PI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
XX WPI; 2003-845253/78.
XX DR N-PSDB; ADF11430.
XX PT New isolated antibody that specifically binds osteoprotegerin ligand,
XX PT useful for diagnosing or treating bone disorders, such as osteoporosis,
XX PT bone loss from arthritis, Paget's disease or osteopenia.
XX PS Claim 18; SEQ ID NO 44; 156pp; English.
XX CC The present invention describes an isolated human antibody (I) that
XX CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
XX CC pharmaceutical composition comprising a pharmaceutical carrier and a
XX CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
XX CC in a patient, comprising administering to a patient the pharmaceutical
XX CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
XX CC for detecting OPGL in a biological sample, comprising contacting the
XX CC sample with (I) under conditions that allow for binding of the antibody
XX CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
XX CC osteopathic, antiarthritic and cytostatic activities, and can be used in
XX CC gene therapy. The composition and methods are useful in diagnosing or
XX CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
XX CC Paget's disease or osteopenia. The antibody (I) may also be used for
XX CC detecting OPGL in biological samples and in identifying cells or tissues
XX CC that produce the protein. The present sequence represents a sequence
XX CC which is used in the exemplification of the present invention.
XX SQ Sequence 214 AA;
Query Match 96.6%; Score 538; DB 7; Length 214;
Best Local Similarity 97.2%; Pred. No. 2.9e-34;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGRVITTCRASQISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGRVITTCRASQISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSVPRTFGQTKVEIK 107
Db 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSVPRTFGQTKVEIK 107
RESULT 9
ADY26773
ID ADY26773 standard; protein; 107 AA.
XX AC ADY26773;
XX DT 19-MAY-2005 (first entry)
XX DE Anti-NGF-antibody light chain variable region SEQ ID NO 88.
XX KW analgesic; gene therapy; antibody engineering; pharmaceutical; pain;
XX KW neurological disease; NGF; nerve growth factor;
XX KW light chain variable region.
XX OS Homo sapiens.
XX PN WO2005019266-A2.
XX PD 03-MAR-2005.
XX PF 15-JUL-2004; 2004WO-US022876.
XX PR 15-JUL-2003; 2003US-0487431P.
XX PA (AMGE-) AMGEN INC.
XX PI Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;
XX WPI; 2005-202606/21.
XX PT New human anti-nerve growth factor (NGF) neutralizing antibodies useful
XX PT for manufacturing a medicament for treating painful disorders (e.g. acute
XX PT pain) or conditions associated with increased expression or sensitivity
XX PT to NGF.
XX PS Claim 33; SEQ ID NO 88; 190pp; English.
XX CC The invention describes an isolated human antibody that interacts with or
XX CC binds specifically to human nerve growth factor (NGF) and neutralize the
XX CC function of NGF. Also described are: methods of treating a condition
XX CC caused by increased expression of NGF or increased sensitivity to NGF in
XX CC a patient; methods for detecting NGF in a biological sample; an NGF
XX CC specific binding agent comprising any of the 59 amino acid sequences
XX CC comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the
XX CC specification, and where the binding agent can bind to NGF; a
XX CC pharmaceutical composition comprising a pharmaceutical carrier and a
XX CC therapeutic amount of the antibody or binding agent cited above; or a
XX CC medicament for treating a painful disorder or condition associated with
XX CC increased expression of NGF or increased sensitivity to NGF, the
XX CC medicament comprising a pharmaceutical amount of a monoclonal antibody or
XX CC its immunologically functional immunoglobulin fragment, or pharmaceutical
XX CC salts of the monoclonal antibody or the fragment, where the monoclonal
XX CC antibody is at least one of the monoclonal antibody cited above, and a
XX CC pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or
XX CC polynucleotide that encodes the above antibody or binding agent; an
XX CC isolated cell line that produces the above antibody or binding agent; an
XX CC expression vector comprising the above polynucleotide; and a host cell
XX CC comprising the nucleic acid or expression vector. The composition
XX CC (including the antibody) and methods are useful for manufacturing a
XX CC medicament for treating a painful disorder (e.g. acute pain, dental pain,
XX CC or pain from trauma or cancer), or a condition associated with increased
XX CC expression of NGF or increased sensitivity to NGF. This is the amino acid
XX CC sequence of a human NGF antibody light chain variable region.
XX SQ Sequence 107 AA;
Query Match 96.4%; Score 537; DB 9; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.8e-34;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGRVITTCRASQISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGRVITTCRASQISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSVPRTFGQTKVEIK 107
Db 61 RFGSGSGTDFTLTISGLQPEDFATYCCQYNSVPRTFGQTKVEIK 107
```


D6 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNSYPWTFGGQTKVEIK 107

RESULT 10

AA072880
ID AA072880 standard; protein; 107 AA.

AC AA072880;

XX 10-MAY-2001 (first entry)

XX Human anti-HER2/neu antibody 3-F2 light chain.

XX Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy; 3-F2;
KW 1-D2; 2-E8; growth factor receptor.

XX Homo sapiens.

XX WO200109187-A2.

XX 08-FEB-2001.

XX 25-JUL-2000; 2000WO-US020272.

XX 29-JUL-1999; 99US-0146313P.

XX 10-MAR-2000; 2000US-0188539P.

XX (MEDA-) MEDAREX INC.

XX Keler T, Deo Y;

XX WPI; 2001-168698/17.

XX N-PSDB; AAF75586.

XX New human monoclonal antibody that specifically binds to growth factor
PT receptor HER2/neu, for treating, preventing or diagnosing diseases
PT characterized by aberrant HER2/neu expression e.g. cancers.

XX Disclosure; Page 104-105; 113pp; English.

XX The present invention provides the protein and coding sequences for human
CC monoclonal antibodies which bind specifically to the HER2/neu growth
CC factor receptor (also known as erbB2). These are designated 3-F2, 1-D2
CC and 2-E8. They can be used in the immunotherapy-based treatment and
CC prognosis of cancers, particularly adenocarcinomas such as salivary
CC gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,
CC and ovarian cancer. The present sequence is part of an antibody of the
CC invention

XX Sequence 107 AA;

Query Match 96.1%; Score 535; DB 4; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.6e-34;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRLAWYQQKPKSLIYAASSLSQGVPS 60

DB 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRLAWYQQKPKSLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNSYPRTFGQTKVEIK 107

DB 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNSYPRTFGQTKLEIK 107

RESULT 11

ADO36490

ID ADO36490 standard; protein; 107 AA.

XX ADO36490;

XX 12-AUG-2004 (first entry)

XX Human anti-heparanase 2H8 Vh amino acid sequence SEQ ID NO:4.

XX

human; monoclonal antibody; heparanase; heparanase inhibitor;
KW anti-heparanase antibody; cytostatic; immunosuppressive; antiarthritic;
KW antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;
KW neuroprotective; nootropic; heparanase antagonist; cancer; tumour;
KW melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;
KW bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;
KW mammary adenocarcinoma; leukaemia; rheumatoid fibroblast;
KW autoimmune disease; arthritis; asthma; lupus erythematosus;
KW allograft rejection; vascular restenosis; atherosclerosis;
KW Alzheimer's disease.

XX Homo sapiens.

XX WO2004043989-A2.

XX 27-MAY-2004.

XX 05-NOV-2003; 2003WO-US035464.

XX 07-NOV-2002; 2002US-0424803P.

XX (MEDA-) MEDAREX INC.

XX (CELL-) CELLTech R & D.

XX Huang H, Holmes S, Mason S;

XX WPI; 2004-411694/38.

XX N-PSDB; ADO36489.

XX New human monoclonal antibody to heparanase, for use in treating or
PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
PT erythematosus, allograft rejection, atherosclerosis, and Alzheimer's
PT disease.

XX Claim 47; SEQ ID NO 4; 109pp; English.

XX The present invention describes an isolated human monoclonal antibody
CC which binds to and inhibits activity of human heparanase. Human anti-
CC heparanase antibodies of the present invention have cytostatic,
CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
CC dermatological, antiarteriosclerotic, neuroprotective and nootropic
CC activities, and can be used as heparanase antagonists. The antibody,
CC methods and compositions of the present invention are useful in treating
CC or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
CC erythematosus, allograft rejection, vascular restenosis, atherosclerosis,
CC and Alzheimer's disease. The present sequence represents a human anti-
CC heparanase 2H8 Vh amino acid sequence, which is used in the
CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 96.1%; Score 535; DB 8; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.6e-34;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRLAWYQQKPKSLIYAASSLSQGVPS 60

DB 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRLAWYQQKPKSLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNSYPRTFGQTKVEIK 107

DB 61 RFGSGSGTDFTLTISLQPEDFATYCCQYNSYPRTFGQTKLEIK 107

RESULT 12

ADO36502

ID ADO36502 standard; protein; 107 AA.

XX

AC ADO36502;

Db 61 RFSGSGGTDFTLTISLQPEDFATYYCQYNSYPYTFGGQTKLEIK 107

RESULT 14

AEBA8576
ID AEB48576 standard; protein; 234 AA.

XX AC AEB48576;

XX DT 06-OCT-2005 (first entry)

XX DE Human kappa light chain-TAKA signal peptide fusion protein.

XX KW monoclonal antibody; antibody production; light chain; alpha amylase;
XX KW TAKA; fusion protein.

XX OS Homo sapiens.

XX OS Aspergillus oryzae.

XX FN WO2005070962-A1.

XX PD 04-AUG-2005.

XX PF 20-JAN-2005; 2005WO-DK000035.

XX PR 21-JAN-2004; 2004DK-00000077.

XX PR 05-FEB-2004; 2004DK-00000174.

XX PR 12-MAY-2004; 2004DK-00000761.

XX PA (NOVO) NOVOZYMES AS.

XX PI Lehmbeck J, Wahlbom F;

XX XX WPI; 2005-533997/54.

XX PT Producing a monoclonal antibody by providing a heterokaryon fungus

XX PT comprising a first nucleus and a second nucleus and culturing the

XX PT heterokaryon fungus for expression of antibody light and heavy chains.

XX PS Example 9; SEQ ID NO 25; 94pp; English.

XX CC The invention describes a method of producing a monoclonal antibody
CC comprising providing a heterokaryon fungus comprising a first nucleus
CC comprising a sequence encoding a light chain of an antibody, and a second
CC nucleus comprising a sequence encoding a heavy chain of an antibody, and
CC culturing the heterokaryon fungus for expression of the antibody light
CC and heavy chains. Also described are: a nucleic acid construct comprising
CC a first nucleic acid sequence encoding a light chain of an antibody and a
CC third nucleic acid sequence encoding a signal peptide heterologous to the
CC first nucleic acid sequence; a nucleic acid construct comprising a first
CC nucleic acid sequence encoding a heavy chain of an antibody and a third
CC nucleic acid sequence encoding a signal peptide heterologous to the first
CC nucleic acid sequence; a nucleic acid construct comprising a first
CC nucleic acid sequence encoding a light chain of an antibody and a second
CC nucleic acid sequence encoding a cellulose binding domain; a nucleic acid
CC construct comprising a first nucleic acid sequence encoding a heavy chain
CC of an antibody and a second nucleic acid sequence encoding a cellulose
CC binding domain; a heterokaryon fungal host cell comprising a first
CC nucleus and a second nucleus, where the first nucleus comprises a first
CC nucleic acid construct comprising a first nucleic acid sequence encoding
CC a light chain of an antibody, and the second nucleus comprises a second
CC nucleic acid construct comprising a first nucleic acid sequence encoding
CC a heavy chain of an antibody, and where at least one of the nucleic acid
CC constructs further comprises a second nucleic acid sequence encoding a
CC polypeptide or a functional part normally secreted by a fungus; and a
CC heterokaryon fungal host cell comprising a first nucleus and a second
CC nucleus, where the first nucleus comprises a first nucleic acid construct
CC comprising a first nucleic acid sequence encoding a light chain of an
CC antibody, and the second nucleus comprises a second nucleic acid
CC construct comprising a first nucleic acid sequence encoding a heavy chain
CC of an antibody, and where at least one of the nucleic acid constructs
CC further comprises a third nucleic acid sequence encoding a signal peptide
CC heterologous to the first nucleic acid sequence. The method is useful for

CC producing monoclonal antibodies in heterokaryon fungus or in fungal host
CC cells. This is the amino acid sequence of a fusion protein comprising
CC human kappa light chain in which the native signal sequence has been
CC replaced with the alpha amylase (TAKA) signal peptide.

XX SQ Sequence 234 AA;

Query Match 96.1%; Score 535; DB 9; Length 234;

Best Local Similarity 96.3%; Pred. No. 5.4e-34;

Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60

Db 21 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 80

Qy 61 RFSGSGGTDFTLTISLQPEDFATYYCQYNSYPYTFGGQTKLEIK 107

Db 81 RFSGSGGTDFTLTISLQPEDFATYYCQYNSYPYTFGGQTKLEIK 127

RESULT 15

ADV86270

ID ADV86270 standard; protein; 236 AA.

XX AC ADV86270;

XX DT 24-FEB-2005 (first entry)

XX DE Anti-human CTGF monoclonal antibody mAb1 light chain protein.

XX KW antibody engineering; immunotherapy; antibody;

XX KW connective tissue growth factor; immunoglobulin; hypertension;

XX KW hypotensive; cardiovascular disease; hyperglycemia; antidiabetic;

XX KW diabetes; metabolic disorder; endocrine disorder;

XX KW congestive heart failure; arthritis; antiarthritic; inflammation;

XX KW antinflammatory; cancer; cytostatic; neoplasm.

XX OS Homo sapiens.

XX PN US2004248206-A1.

XX PD 09-DEC-2004.

XX PF 01-JUN-2004; 2004US-00858186.

XX PR 04-JUN-2003; 2003US-0475598P.

XX PA (LINA/) LIN A Y.

XX PA (NEFF/) NEFF T B.

XX PA (OLIV/) OLIVER N A.

XX PA (USIN/) USINGER W R.

XX PA (WANG/) WANG Q.

XX PA (YEOW/) YEOWELL D A.

XX PI Lin AY, Neff TB, Oliver NA, Usinger WR, Wang Q, Yeowell DA;

XX WPI; 2005-072821/08.

XX DR N-PSDB; ADV86269.

XX Novel isolated antibody specifically binding to connective tissue growth
PT factor (CTGF), useful for neutralizing activity associated with CTGF and
PT treating CTGF-associated disorder such as hypertension, hyperglycemia or
PT diabetes.

XX Claim 32; SEQ ID NO 20; 54pp; English.

XX The invention relates to an isolated antibody or its fragment that
CC specifically binds to connective tissue growth factor (CTGF) polypeptide
CC having at least a portion of sequence of 62 amino acids fully defined in
CC specification, or of an orthologous polypeptide derived from non-human
CC species, having immunoglobulin sequence of 469 or 236 amino acids fully
CC defined in specification, or antibody produced by cell line identified by
CC ATCC accession number PTA-6006. (I) is useful for neutralizing an

CC activity associated with CTGF, which involves contacting (I) with a CTGF
 CC polypeptide in vitro or in vivo in a subject, under conditions suitable
 CC for formation of a complex comprising the antibody and the CTGF
 CC polypeptide, thus neutralizing the activity associated with CTGF. The
 CC subject has hypertension, hyperglycemia, diabetes, congestive heart
 CC failure, arthritis, and local or systemic inflammation. The subject has
 CC or is at risk for having a CTGF-associated disorder such as cancer. The
 CC cancer is chosen from acute lymphoblastic leukemia, dermatofibromas,
 CC breast cancer, breast carcinoma desmoplasia, angiolipoma, angioleiomyoma,
 CC desmoplastic cancer, prostate cancer, ovarian cancer, colorectal cancer,
 CC pancreatic cancer, gastrointestinal cancer, and liver cancer. The CTGF-
 CC associated disorder is a fibrotic disorder chosen from idiopathic
 CC pulmonary fibrosis, kidney fibrosis, glomerular sclerosis, ocular
 CC fibrosis, osteoarthritis, scleroderma, cardiac fibrosis, or liver
 CC fibrosis. (I) is useful for treating or preventing a CTGF-associated
 CC disorder in a subject having or at risk for having the disorder, which
 CC involves administering (I) to the subject. The subject is at risk due to
 CC a condition chosen from hypertension, hyperglycemia, diabetes, myocardial
 CC infarction, arthritis, and inflammation. The CTGF-associated disorder is
 CC chosen from diabetic nephropathy, diabetic retinopathy, and diabetic
 CC cardiovascular disease, or cancer. (II) is useful for treating CTGF-
 CC associated disorders (claimed). (I) is useful for quantitatively and
 CC qualitatively detecting CTGF in a sample, diagnosing disease or disorder
 CC associated with CTGF, identifying whether or not an individual has a
 CC predisposition to develop a CTGF-associated disorder, and for monitoring
 CC the therapeutic efficacy of treatment of a CTGF-associated disorder, and
 CC also as affinity purification agents. This sequence corresponds to the
 CC anti-human CTGF protein monoclonal antibody light chain protein.
 XX

Sequence 236 AA;

Query Match 96.1%; Score 535; DB 9; Length 236;
 Best Local Similarity 96.3%; Pred. No. 5.5e-34;
 Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
 Db 23 DIQMTQSPSSLSASVGRVTITCRASQGISRLAWYQOKPEKAPKSLIYAASSLSQGVPS 82
 Qy 61 RFGSGSGGTDFLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 107
 Db 83 RFGSGSGGTDFLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 129

Search completed: December 3, 2005, 14:25:03
 Job time : 184.992 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:59 ; Search time 29.2612 Seconds
(without alignments)
351.837 Million cell updates/sec

Title: US-10-769-144-8
Perfect score: 557
Sequence: 1 DIQMTQSPSSLSASVGRVT.....CQYNSYPRTFGQTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500	89.8	125	2 S40333	Ig kappa chain V-J
2	496	89.0	107	2 T69017	anti-HIV1 envelope
3	491	88.2	129	2 S40369	Ig kappa chain - h
4	489	87.8	131	2 S40352	Ig kappa chain V-J
5	486	87.3	117	2 S46376	Ig kappa chain V-J
6	485	87.1	123	2 S40331	Ig kappa chain - h
7	484	86.9	117	2 B21056	Ig kappa chain pre
8	483	86.7	128	2 S46372	Ig light chain var
9	480	86.2	117	2 S46371	Ig kappa chain V-J
10	480	86.2	125	2 S40353	Ig kappa chain V-J
11	479	86.0	117	1 K1HU11	Ig kappa chain pre
12	479	86.0	123	2 S40313	Ig kappa chain V-J
13	479	86.0	125	2 S40349	Ig kappa chain V-J
14	478	85.8	132	2 S38646	Ig kappa chain V r
15	476	85.5	108	1 K1HUGL	Ig kappa chain V-I
16	476	85.5	141	2 A49134	Ig kappa chain V-I
17	474.5	85.2	107	2 S47183	Ig kappa chain - h
18	474.5	85.2	124	2 S40336	Ig kappa chain V-J
19	474	85.1	108	1 K1HUEN	Ig kappa chain V-I
20	474	85.1	127	2 S11240	Ig kappa chain V r
21	473	84.9	132	2 S40334	Ig kappa chain - h
22	472.5	84.8	107	2 S36275	Ig kappa chain V
23	472	84.7	108	2 S36264	Ig lambda chain V
24	471	84.6	107	2 B49047	Ig kappa chain V r
25	471	84.6	127	2 S40367	Ig kappa chain V-J
26	469	84.2	124	2 S40318	Ig kappa chain - h
27	469	84.2	125	2 S40316	Ig kappa chain V r
28	468	84.0	108	1 K1HUEU	Ig kappa chain V-I
29	467	83.8	108	1 K1HUKU	Ig kappa chain V-I

30	466	83.7	108	2 S36277	Ig lambda chain V
31	466	83.7	122	2 S40370	Ig kappa chain - h
32	465	83.5	108	1 K1HUWE	Ig kappa chain V-I
33	465	83.5	108	2 S36279	Ig lambda chain V
34	465	83.5	117	2 C21056	Ig kappa chain pre
35	465	83.5	130	2 S40368	Ig kappa chain - h
36	462	82.9	108	2 S19674	Ig kappa chain V r
37	461.5	82.9	108	2 S30521	Ig kappa chain V r
38	461	82.8	107	2 S36262	Ig lambda chain V
39	460	82.6	107	2 S36269	Ig lambda chain V
40	459	82.4	108	1 K1HUUH	Ig kappa chain V-I
41	458	82.2	110	2 PNO535	Ig kappa chain V r
42	457.5	82.1	107	1 K1HUAR	Ig kappa chain V-I
43	457.5	82.1	108	2 S34007	Ig kappa chain V r
44	457	82.0	105	2 S36266	Ig lambda chain V
45	456	81.9	108	1 K1HUAG	Ig kappa chain V-I

ALIGNMENTS

RESULT 1
S40333
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40333
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40333
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: UNIPARC:UPI0000116153; EMBL:X72443; NID:9441354; PIDN:CAA51111.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 500; DB 2; Length 125;
Best Local Similarity 89.7%; Pred. No. 1.4e-36;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVTITCRASQISGLAWYQQKPEKAPKSLIYAASSLQSGVPS 60
Db 19 DIQMTQSPSTLSASVGRVTITCRASQISGLAWYQQKPEKAPKSLIYKASSLESQVPS 78
Qy 61 RFSGSGSGTDFTLTISGLQPEDFATYYCQQYNISYPRTFGQTKVEIK 107
Db 79 RFSGSGSGTEFTLTITISLQPDFATYYCQQYNISYPRTFGQTKVEIK 125

RESULT 2
T69017
anti-HIV1 envelope protein gp120 V3 loop monoclonal antibody L chain V region - human (F
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C;Accession: T69017
R;Chin, L.T.; Duenas, M.; Levi, M.; Hinkula, J.; Wahren, B.; Borrebaeck, C.A.
Immunol. Lett. 44, 25-30, 1995
A;Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed a
A;Reference number: I54563; MUID:95237884; PMID:7721339
A;Accession: T69017
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-107 <RES>
A;Cross-references: UNIPARC:UPI0000113F9C; GB:S77140; NID:9913352; PIDN:AAB34102.1; PID:
C;Genetics:
A;Gene: Ig V kappa
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

```
Query Match      89.0%; Score 496; DB 2; Length 107;
Best Local Similarity 90.7%; Pred. No. 2.7e-38;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASHDIOGSLAWYQOKPEKAPESLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKVEIK 107
Db 61 RFGSGSGTDFTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKVLIK 107

RESULT 3
S40369
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40369
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40369
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-129 <KLE>
A/Cross-references: UNIPARC:UPI0000116177; EMBL:X72479; NID:9441426; PIDN:CAA51147.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/37-111/Domain: immunoglobulin homology <IMM>

Query Match      88.2%; Score 491; DB 2; Length 129;
Best Local Similarity 89.7%; Pred. No. 9.2e-38;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 22 DIQWTQSPSSLSASVGDRTVITCRASHVISHNLVWFQOKPKAPKSLIYAASSLSQGVPS 81

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKVEIK 107
Db 82 KFGSGSGTDFTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKLEIK 128

RESULT 4
S40352
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40352
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40352
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-131 <KLE>
A/Cross-references: UNIPARC:UPI0000116166; EMBL:X72462; NID:9441392; PIDN:CAA51130.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/36-110/Domain: immunoglobulin homology <IMM>

Query Match      87.8%; Score 489; DB 2; Length 131;
Best Local Similarity 88.8%; Pred. No. 1.4e-37;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 21 DIQWTQSPSSLSASVGNRTVITCRASQGISNLYAWYQOKPKVPLIYAASLTLSQGVPS 80

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKVEIK 107
```

```
Db 81 RFGSGSGTDFSLTISGLQPEDVATYYCQYNSVPRTFGGQTKVEIK 127

RESULT 5
S46376
Ig kappa chain V-J region (T33-14) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C/Accession: S46376; S38649
R/Bensimon, C.; Chaetagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A/Reference number: S46369; MUID:94313975; PMID:8039491
A/Accession: S46376
A/Molecule type: mRNA
A/Residues: 1-117 <BEN>
A/Cross-references: UNIPARC:UPI00001165A9; EMBL:Z27177; NID:9415969; PIDN:CAA81701.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/25-99/Domain: immunoglobulin homology <IMM>

Query Match      87.3%; Score 486; DB 2; Length 117;
Best Local Similarity 87.9%; Pred. No. 2.4e-37;
Matches 94; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 10 DIQWTQSPSSVSASIGDRTVITCRASQDISSWLAWYQOKPKAPKLIYAASSLSQGVPL 69

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKVEIK 107
Db 70 RFGSGSGTDFTLTISGLQPEDFATYYCCQANSFPRGFGPTKVDIK 116

RESULT 6
S40331
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40331
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40331
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-123 <KLE>
A/Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/32-106/Domain: immunoglobulin homology <IMM>

Query Match      87.1%; Score 485; DB 2; Length 123;
Best Local Similarity 90.7%; Pred. No. 3.1e-37;
Matches 97; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 17 DIQWTQSPSSLSASVGDRTVITCRASQSISSYLNWYQOKPKAPKLIYAASSLSQGVPS 76

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCCQYNSYPRTFGGQTKVEIK 107
Db 77 RFGSGSGTDFTLTISGLQPEDFATYYCCQYSYSPRTFPGQTKVEIK 123

RESULT 7
B21056
Ig kappa chain precursor V region (HK134) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000
C/Accession: B21056
```

R;Bentley, D.L.; Rabbitts, T.H.
Cell 32, 181-189, 1983
A:Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicated
A:Reference number: A21056; MUID:83129397; PMID:6402305
A:Accession: B21056
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <BEN>
A:Cross-references: UNIPARC:UPI0000116772; GB:K01323; NID:g185995; PIDN:AAA58931.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 484; DB 2; Length 117;
Best Local Similarity 97.9%; Pred. No. 3.6e-37;
Matches 93; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQSGVPS 82
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYP 95
Db 83 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYP 117

RESULT 8
S46372
Ig light chain variable region (VJ) - human
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S46372
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46372
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <BEN>
A:Cross-references: UNIPARC:UPI0000176CA4; EMBL:227173
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 86.7%; Score 483; DB 2; Length 128;
Best Local Similarity 89.6%; Pred. No. 4.8e-37;
Matches 95; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 IQMTQSPSSLSASVGDRTVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQSGVPSR 61
Db 22 IIRITQSPSSLSASTGDRVTITTCRASQGISRWLAAYQOKPGKAPKLLIYAASLTQSGVPSR 81
Qy 62 FSGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 107
Db 82 FSGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 127

RESULT 9
S46371
Ig kappa chain V-J region (T24-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46371; S38645
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46371
A:Molecule type: mRNA
A:Residues: 1-117 <BEN>
A:Cross-references: UNIPARC:UPI00001165A4; EMBL:227172; NID:g415959; PIDN:CAA81696.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:23-97/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 480; DB 2; Length 117;
Best Local Similarity 85.3%; Pred. No. 8.3e-37;
Matches 93; Conservative 7; Mismatches 7; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 8 DIQMTQSPSTLSASVGDRTVITTCRASRSISTWLAWYQOKPGKAPKLLIYKASTLESQVPS 67
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSY--PRTFQGTKEIK 107
Db 68 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYFPYTFQGTKEIK 116

RESULT 10
S40353
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40353
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40353
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: UNIPARC:UPI0000176CAE; EMBL:X72463
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 480; DB 2; Length 125;
Best Local Similarity 87.9%; Pred. No. 8.9e-37;
Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 15 DIQMTQSPSSLSASVGDRTVITTCRASQGISRWLAAYQOKPGKAPKRLIYAASSFSQSGVPS 74
Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFQGTKEIK 107
Db 75 RFGSGSGTDFTLTISGLQPEDFATYYCLOHNSYPLTFGGGTKEIK 121

RESULT 11
K1HUI1
Ig kappa chain precursor V-I region (HK101) - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 09-Jul-2004
C:Accession: A01881; A21056
R;Bentley, D.L.; Rabbitts, T.H.
Nature 288, 730-733, 1980
A:Title: Human immunoglobulin variable region genes - DNA sequences of two V-kappa genes
A:Reference number: A93241; MUID:81098966; PMID:6779204
A:Accession: A01881
A:Molecule type: DNA
A:Residues: 1-117 <BEN1>
A:Cross-references: UNIPROT:P01601; UNIPARC:UPI000012E144; GB:V00558; GB:J00244; GB:J002
A:Note: the sequence was determined from the germline gene
R;Bentley, D.L.; Rabbitts, T.H.
Cell 32, 181-189, 1983
A:Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicat
A:Reference number: A21056; MUID:83129397; PMID:6402305
A:Accession: A21056
A:Molecule type: DNA
A:Residues: 1-117 <BEN2>
A:Cross-references: UNIPARC:UPI000012E144; GB:K01322; NID:g185993; PIDN:AAA58930.1; PID
C:Genetics:
A:Gene: GDB:IGKV1

A;Cross-references: GDB:l36264
A;Map position: 2p12-2p12
A;Introns: 19/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-117/Product: Ig kappa chain V-I region (HK101) #status predicted <MAT>
F;38-112/Domain: immunoglobulin homology <IMM>
F;45-110/Disulfide bonds: #status predicted

Query Match 86.0%; Score 479; DB 1; Length 117;
Best Local Similarity 96.8%; Pred. No. 1.e-36; Mismatches 0; Indels 0; Gaps 0;
Matches 92; Conservative 0

Qy 1 DIQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 23 DIQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPS 82

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYP 95
Db 83 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYP 117

RESULT 12
S40313
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40313
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40313
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <KLE>
A;Cross-references: UNIPARC:UPI000011613F; EMBL:X72423; NID:g441314; PIDN:CAA51091.1; PI10000011613
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 479; DB 2; Length 123;
Best Local Similarity 87.9%; Pred. No. 1.e-36; Mismatches 3; Indels 0; Gaps 0;
Matches 94; Conservative 3

Qy 1 DIQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPS 60
Db 17 DIQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPS 76

Qy 61 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 107
Db 77 RFGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 123

RESULT 13
S40349
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S40349
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40349
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: UNIPARC:UPI0000116163; EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PI10000011616
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 479; DB 2; Length 125;
Best Local Similarity 88.7%; Pred. No. 1.e-36; Mismatches 4; Indels 0; Gaps 0;
Matches 94; Conservative 4

Qy 2 IQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPSR 61
Db 19 IQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPSR 78

Qy 62 FSGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 107
Db 79 FSGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 124

RESULT 14
S38646
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38646
R;Bensimon, C.; Chastagner, P.; Zouali, M.
submitted to the EMBL Data Library, November 1993
A;Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A;Reference number: S38643
A;Accession: S38646
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <BEN>
A;Cross-references: UNIPARC:UPI00001165A5; EMBL:Z27173; NID:g415961; PIDN:CAA81697.1; PI1000001165A
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;40-114/Domain: immunoglobulin homology <IMM>

Query Match 85.8%; Score 478; DB 2; Length 132;
Best Local Similarity 88.7%; Pred. No. 1.e-36; Mismatches 8; Indels 0; Gaps 0;
Matches 94; Conservative 4

Qy 2 IQNTQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPSR 61
Db 26 IRTAQSPSSLSASVGRVITTCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQGVPSR 85

Qy 62 FSGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 107
Db 86 FSGSGSGTDFTLTISGLQPEDFATYYCQYNSYPRTFGQGTKEIK 131

RESULT 15
K1HUGL
Ig kappa chain V-I region (Gal) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01867
R;Laure, C.J.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973
A;Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), I
A;Reference number: A01867; MUID:75059122; PMID:4215718
A;Accession: A01867
A;Molecule type: protein
A;Residues: 1-108 <LAU>
A;Cross-references: UNIPROT:P01599; UNIPARC:UPI0000012E142
A;Note: the C region of this chain has the Inv (3) marker
C;Comment: This chain was isolated from a Waldenstrom's macroglobulin.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:l36264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>

F;23-88/Disulfide bonds: #status predicted

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Query Match      85.5%; Score 476; DB 1; Length 108;
Best Local Similarity 86.9%; Pred. No. 1.8e-36;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy      1 DIQMTQSPSSLSASVGDRTTITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60
Db      1 DIQMTQSPSSLSASVGDRTTITCRASQGISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60

Qy      61 RFSGSGGTDFLTITISGLQPEDFATYCCQYNSYPRTEFGQTKVEIK 107
Db      61 RFSGSGGTDFLTITISGLQPEDFATYCCQYNSYPRTEFGQTKVEIK 107
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Search completed: December 3, 2005, 14:33:32
Job time : 29.2612 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:24:58 ; Search time 45.4204 Seconds
(without alignments)
194.765 Million cell updates/sec

Title: US-10-769-144-8

Perfect score: 557

Sequence: 1 DIQWTSFSSLSASVGRVT.....CQQNSYPTFGQTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5-COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6-COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H-COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCRTUS-COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	529	95.0	108	2	US-09-920-262A-8
2	499	89.6	107	1	US-07-934-373C-18
3	499	89.6	107	2	US-08-437-642B-18
4	499	89.6	107	2	US-08-146-206C-18
5	499	89.6	107	2	US-09-648-067A-14
6	499	89.6	107	2	US-09-705-686-18
7	499	89.6	107	2	US-09-705-392A-18
8	499	89.6	107	2	US-09-705-398-18
9	499	89.6	107	2	US-09-602-812A-5
10	499	89.6	107	4	PCT-US93-07832-18
11	499	89.6	108	2	US-08-974-899-3
12	499	89.6	108	2	US-09-795-798-3
13	499	89.6	108	2	US-08-908-469-12
14	497	89.2	109	1	US-07-934-373C-3
15	497	89.2	109	1	US-08-437-642B-3
16	497	89.2	109	2	US-08-146-206C-3
17	497	89.2	109	2	US-09-705-686-3
18	497	89.2	109	2	US-09-705-392A-3
19	497	89.2	109	2	US-09-705-398-3
20	497	89.2	109	4	PCT-US93-07832-3
21	497	89.2	236	2	US-09-859-053-30
22	491	88.2	109	2	US-09-025-769B-28
23	491	88.2	109	2	US-09-025-769B-43
24	491	88.2	109	2	US-09-490-070A-28
25	491	88.2	109	2	US-09-490-070A-43
26	491	88.2	109	2	US-09-490-153-28
27	491	88.2	109	2	US-09-490-153-43

28	491	88.2	109	2	US-09-490-324-28	Sequence 28, Appl
29	491	88.2	109	2	US-09-490-324-43	Sequence 43, Appl
30	488	87.6	108	2	US-08-974-899-2	Sequence 2, Appl
31	488	87.6	108	2	US-09-795-798-2	Sequence 2, Appl
32	486	87.3	107	2	US-10-330-613A-18	Sequence 18, Appl
33	484	86.9	107	2	US-08-599-226-1	Sequence 1, Appl
34	484	86.9	107	2	US-08-125-098-1	Sequence 1, Appl
35	484	86.9	107	2	US-09-540-018-1	Sequence 1, Appl
36	484	86.9	117	2	US-09-042-353-48	Sequence 48, Appl
37	484	86.9	117	2	US-08-758-417A-313	Sequence 313, App
38	483	86.7	107	2	US-08-599-226-9	Sequence 9, Appl
39	483	86.7	107	2	US-09-125-098-9	Sequence 9, Appl
40	483	86.7	107	2	US-09-540-018-9	Sequence 9, Appl
41	482	86.5	109	2	US-09-157-370-3	Sequence 3, Appl
42	481.5	86.4	109	2	US-09-798-058-4	Sequence 4, Appl
43	481	86.4	107	1	US-08-276-852-84	Sequence 84, Appl
44	481	86.4	107	1	US-08-899-575-84	Sequence 84, Appl
45	481	86.4	107	1	US-08-899-575-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1
US-09-920-262A-8
; Sequence 8, Application US/09920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallon, Bernie
; APPLICANT: Gilles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920.262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-8

Query Match	95.0%	Score 529;	DB 2;	Length 108;
Best Local Similarity	95.3%	Pred. No. 1.8e-44;		
Matches 102;	Conservative 1;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	DIQWTSFSSLSASVGRVTITCRASQISRWLAWYQOKPEKAPKSLIYAASLSQGVPS	60	
Db	1	DIQWTSFSSLSASVGRVTITCRASQISRWLAWYQOKPEKAPKSLIYAASLSQGVPS	60	
Qy	61	RFSGSGSGTDTLTITSGLOPEDEATYCCQNSYPTFGQTKVEIK	107	
Db	61	RFSGSGSGTDTLTITSGLOPEDEATYCCQNSYPTFGQTKVEIK	107	

RESULT 2
US-07-934-373C-18
; Sequence 18, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

```

; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934.373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-07-934-373C-18
Query Match 89.6%; Score 499; DB 1; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNYSYPRTFGGQTKVEIK 107
Db 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNYSYPRTFGGQTKVEIK 107

RESULT 3
US-08-437-642B-18
; Sequence 18, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437.642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
;
US-08-437-642B-18
Query Match 89.6%; Score 499; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNYSYPRTFGGQTKVEIK 107
Db 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNYSYPRTFGGQTKVEIK 107

RESULT 4
US-08-146-206C-18
; Sequence 18, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146.206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
;
US-08-146-206C-18
Query Match 89.6%; Score 499; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNYSYPRTFGGQTKVEIK 107
Db 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNYSYPRTFGGQTKVEIK 107
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; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-146-206C-18

Query Match      89.6%; Score 499; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIYAASSLSQGVPS 60
   |||||
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIYAASSLSQGVPS 60
   |||||

Qy 61 RFGSGSGTDFLTITISGLQPEDPATYQCQYNSYPRTFGGTKVEIK 107
   |||||
Db 61 RFGSGSGTDFLTITISGLQPEDPATYQCQYNSLPTWTFGGTKVEIK 107
   |||||

RESULT 5
US-09-648-067A-14
; Sequence 14, Application US/09648067A
; Patent No. 6627196
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P175R1
; CURRENT APPLICATION NUMBER: US/09/648,067A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VL consensus sequence
US-09-648-067A-14

Query Match      89.6%; Score 499; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIYAASSLSQGVPS 60
   |||||
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIYAASSLSQGVPS 60
   |||||

Qy 61 RFGSGSGTDFLTITISGLQPEDPATYQCQYNSYPRTFGGTKVEIK 107
   |||||
Db 61 RFGSGSGTDFLTITISGLQPEDPATYQCQYNSLPTWTFGGTKVEIK 107
   |||||

RESULT 6
US-09-705-686-18
; Sequence 18, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

Query Match      89.6%; Score 499; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIYAASSLSQGVPS 60
   |||||
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIYAASSLSQGVPS 60
   |||||

Qy 61 RFGSGSGTDFLTITISGLQPEDPATYQCQYNSYPRTFGGTKVEIK 107
   |||||
Db 61 RFGSGSGTDFLTITISGLQPEDPATYQCQYNSLPTWTFGGTKVEIK 107
   |||||

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709PID3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18

Query Match      89.6%; Score 499; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIYAASSLSQGVPS 60
   |||||
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISRWLAWYQQKPKAPKSLIYAASSLSQGVPS 60
   |||||

Qy 61 RFGSGSGTDFLTITISGLQPEDPATYQCQYNSYPRTFGGTKVEIK 107
   |||||
Db 61 RFGSGSGTDFLTITISGLQPEDPATYQCQYNSLPTWTFGGTKVEIK 107
   |||||

RESULT 7
US-09-705-392A-18
; Sequence 18, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-No. 6719971-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
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/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 40,378
/ REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1994
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-392A-18

Query Match      89.6%; Score 499; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQSGVPS 60
   |||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQSGVPS 60
   |||||

Qy 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPRTFGGQTKVEIK 107
   |||||
Db 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPRTFGGQTKVEIK 107
   |||||

RESULT 9
US-09-602-812A-5
/ Sequence 5, Application US/09602812A
/ Patent No. 6949245
/ GENERAL INFORMATION:
/ APPLICANT: Adams, Camellia W.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Sliwowski, Mark X.
/ TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with
/ TITLE OF INVENTION: Anti-ErbB2 Antibodies
/ FILE REFERENCE: P1467R2
/ CURRENT APPLICATION NUMBER: US/09/602,812A
/ CURRENT FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 60/141,316
/ PRIOR FILING DATE: 1999-06-25
/ NUMBER OF SEQ ID NOS: 13
/ SEQ ID NO 5
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: light chain consensus sequence
US-09-602-812A-5

Query Match      89.6%; Score 499; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQSGVPS 60
   |||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAAYQOKPEKAPKSLIYAASSLSQSGVPS 60
   |||||

Qy 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPRTFGGQTKVEIK 107
   |||||
Db 61 RFGSGSGTDTLTISGLQPEDFATYYCQYNSYPRTFGGQTKVEIK 107
   |||||

RESULT 10
PCT-US93-07832-18
/ Sequence 18, Application PC/TUS9307832
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ TITLE OF INVENTION: Immunoglobulin Variants
/ NUMBER OF SEQUENCES: 40
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/705,398
/ FILING DATE: 02-NOV-1993
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/146206
/ FILING DATE: 17-NOV-1993
/ APPLICATION NUMBER: 07/715272
/ FILING DATE: 14-JUN-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 40,378
/ REFERENCE/DOCKET NUMBER: P0709P1D2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1994
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-398-18

Query Match      89.6%; Score 499; DB 2; Length 107;
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; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US93-07832-18

Query Match 89.6%; Score 499; DB 4; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Qy 61 RFGSGSGTDTLTITISGLQPEDFATYYCQQYNSYPRTFGGQTKVEIK 107
Db 61 RFGSGSGTDTLTITISGLQPEDFATYYCQQYNSYPRTFGGQTKVEIK 107

RESULT 11
US-08-974-899-3
; Sequence 3, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE: 11/27/96
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-974-899-3

Query Match 89.6%; Score 499; DB 2; Length 108;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Qy 61 RFGSGSGTDTLTITISGLQPEDFATYYCQQYNSYPRTFGGQTKVEIK 107
Db 61 RFGSGSGTDTLTITISGLQPEDFATYYCQQYNSYPRTFGGQTKVEIK 107

RESULT 12
US-09-795-798-3
; Sequence 3, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; APPLICATION NUMBER: US/09/795-798-3
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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Query Match 89.6%; Score 499; DB 2; Length 108;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Qy 61 RFGSGSGTDTLTITISGLQPEDFATYYCQQYNSYPRTFGGQTKVEIK 107
Db 61 RFGSGSGTDTLTITISGLQPEDFATYYCQQYNSYPRTFGGQTKVEIK 107
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RESULT 13

US-08-908-469-12
; Sequence 12, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/225-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-908-469-12

Query Match 89.6%; Score 499; DB 2; Length 108;
Best Local Similarity 91.6%; Pred. No. 1.5e-41;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQWTQSPSSLSASVGDRTVITCRASQISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60
DB 1 DIQWTQSPSSLSASVGDRTVITCRASQISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60
QY 61 RFGSGSGTDTLTITISLQPEDFATYCCQYNSYPRTFGGTKVEIK 107
DB 61 RFGSGSGTDTLTITISLQPEDFATYCCQYNSLPTWTFGGTKVEIK 107

RESULT 14

US-07-934-373C-3
; Sequence 3, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco

; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-AUG-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-3

Query Match 89.2%; Score 497; DB 1; Length 109;
Best Local Similarity 90.7%; Pred. No. 2.4e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQWTQSPSSLSASVGDRTVITCRASQISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60
DB 1 DIQWTQSPSSLSASVGDRTVITCRASQISRWLAHYQOKPEKAPKSLIYAASSLSQGVPS 60
QY 61 RFGSGSGTDTLTITISLQPEDFATYCCQYNSYPRTFGGTKVEIK 107
DB 61 RFGSGSGTDTLTITISLQPEDFATYCCQYNSLPTWTFGGTKVEIK 107

RESULT 15

US-08-437-642B-3
; Sequence 3, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-3

Query Match      89.2%; Score 497; DB 2; Length 109;
Best Local Similarity 90.7%; Pred. No. 2.4e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGISRWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDVSSILAWYQOKPEKAPKLLIYAASSLESQVPS 60

Qy 61 RFGSGSGCTDFTLTISGLQPEDFATYYCQYNSYPRTFGQGTKVEIK 107
Db 61 RFGSGSGCTDFTLTISGLQPEDFATYYCQYNSLPTFTFGQGTKVEIK 107
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Search completed: December 3, 2005, 14:11:29
Job time : 46.4204 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 13:24:58 ; Search time 49.2408 Seconds
(without alignments)
194.765 Million cell updates/sec

Title: US-10-769-144-4

Perfect score: 621

Sequence: 1 EVQLVQSGAEVKKPGESLR.....TRGDRGVDMGQGLTVTVSS 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep:*
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- 4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	89.5	120	2	US-09-025-769B-40 Sequence 40, Appl
2	556	89.5	120	2	US-09-025-769B-67 Sequence 67, Appl
3	556	89.5	120	2	US-09-490-070A-40 Sequence 40, Appl
4	556	89.5	120	2	US-09-490-070A-67 Sequence 67, Appl
5	556	89.5	120	2	US-09-490-153-40 Sequence 40, Appl
6	556	89.5	120	2	US-09-490-153-67 Sequence 67, Appl
7	556	89.5	120	2	US-09-490-324-40 Sequence 40, Appl
8	556	89.5	120	2	US-09-490-324-67 Sequence 67, Appl
9	553.5	89.1	119	2	US-09-025-769B-26 Sequence 26, Appl
10	553.5	89.1	119	2	US-09-490-070A-26 Sequence 26, Appl
11	553.5	89.1	119	2	US-09-490-153-26 Sequence 26, Appl
12	553.5	89.1	119	2	US-09-490-324-26 Sequence 26, Appl
13	505.5	81.4	119	2	US-09-920-262A-7 Sequence 7, Appl
14	496.5	80.0	129	1	US-08-665-202-32 Sequence 32, Appl
15	496.5	80.0	129	2	US-09-315-574-32 Sequence 32, Appl
16	496.5	80.0	258	1	US-08-665-202-5 Sequence 5, Appl
17	496.5	80.0	258	2	US-09-315-574-5 Sequence 5, Appl
18	496.5	80.0	262	2	US-09-069-821-4 Sequence 4, Appl
19	496.5	80.0	262	2	US-09-956-086-4 Sequence 4, Appl
20	496.5	80.0	262	2	US-09-956-087-4 Sequence 4, Appl
21	496.5	80.0	282	2	US-09-420-592A-7 Sequence 7, Appl
22	496.5	80.0	282	2	US-09-985-442-7 Sequence 7, Appl
23	496.5	80.0	282	2	US-09-983-580-7 Sequence 7, Appl
24	495	79.7	98	1	US-08-665-202-33 Sequence 33, Appl
25	495	79.7	98	2	US-09-315-574-33 Sequence 33, Appl
26	495	79.7	98	2	US-10-194-975-45 Sequence 45, Appl
27	495	79.7	117	2	US-08-545-809A-133 Sequence 133, Appl

28	495	79.7	117	2	US-09-515-697-133 Sequence 133, App
29	494.5	79.6	111	2	US-09-726-219A-171 Sequence 171, App
30	494.5	79.6	111	2	US-09-196-522-171 Sequence 171, App
31	490	78.9	98	1	US-08-478-039-81 Sequence 81, Appl
32	490	78.9	98	1	US-08-476-349A-81 Sequence 81, Appl
33	488.5	78.7	125	1	US-08-665-202-56 Sequence 56, Appl
34	488.5	78.7	125	2	US-09-315-574-56 Sequence 56, Appl
35	484.5	78.0	125	1	US-08-665-202-59 Sequence 59, Appl
36	484.5	78.0	125	2	US-09-315-574-59 Sequence 59, Appl
37	483.5	77.9	125	1	US-08-665-202-53 Sequence 53, Appl
38	483.5	77.9	125	2	US-08-665-202-54 Sequence 54, Appl
39	483.5	77.9	125	1	US-09-315-574-53 Sequence 53, Appl
40	483.5	77.9	125	2	US-09-315-574-54 Sequence 54, Appl
41	481.5	77.5	125	1	US-08-665-202-45 Sequence 45, Appl
42	481.5	77.5	125	2	US-08-665-202-46 Sequence 46, Appl
43	481.5	77.5	125	1	US-08-665-202-48 Sequence 48, Appl
44	481.5	77.5	125	2	US-08-665-202-55 Sequence 55, Appl
45	481.5	77.5	125	2	US-09-315-574-45 Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-40
; Sequence 40, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Pluckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-40

Query Match 89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDPTFTYWGVRQMPGKGLVWGGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDPTFTYWGVRQMPGKGLVWGGIIYPGDSDTIY 60
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSLKSASDTAMYCTR---GDRGVVDYWGQGLTLVTSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSLKSASDTAMYCTR---GDRGVVDYWGQGLTLVTSS 120

RESULT 2

US-09-025-769B-67
; Sequence 67, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/S
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-025-769B-67

Query Match 89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDPTFTYWGVRQMPGKGLVWGGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDPTFTYWGVRQMPGKGLVWGGIIYPGDSDTIY 60
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSLKSASDTAMYCTR---GDRGVVDYWGQGLTLVTSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSLKSASDTAMYCTR---GDRGVVDYWGQGLTLVTSS 120

RESULT 3

US-09-490-070A-40
; Sequence 40, Application US/09490070A
; Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-490-070A-40

Query Match 89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDPTFTYWGVRQMPGKGLVWGGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDPTFTYWGVRQMPGKGLVWGGIIYPGDSDTIY 60
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSLKSASDTAMYCTR---GDRGVVDYWGQGLTLVTSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSLKSASDTAMYCTR---GDRGVVDYWGQGLTLVTSS 120

RESULT 4

US-09-490-070A-67
; Sequence 67, Application US/09490070A
; Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

White & McAlliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-070A-67
Query Match 89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
QY 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPGKGLWMGIIYPGDSDTYI 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPGKGLWMGIIYPGDSDTYI 60
QY 61 SPSPFGQVTTISADKSIISTAYLQWSSLKASDTAMYCYCTR-----GDRGVYWGQGTLLVTSS 116
Db 61 SPSPFGQVTTISADKSIISTAYLQWSSLKASDTAMYCYCTR-----GDRGVYWGQGTLLVTSS 120
RESULT 5
US-09-490-153-40
Sequence 40, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-153-40
Query Match 89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
QY 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPGKGLWMGIIYPGDSDTYI 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPGKGLWMGIIYPGDSDTYI 60
QY 61 SPSPFGQVTTISADKSIISTAYLQWSSLKASDTAMYCYCTR-----GDRGVYWGQGTLLVTSS 116
Db 61 SPSPFGQVTTISADKSIISTAYLQWSSLKASDTAMYCYCTR-----GDRGVYWGQGTLLVTSS 120
RESULT 6
US-09-490-153-67
Sequence 67, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

```
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)596-9000
/ TELEFAX: (212)596-9090
/ INFORMATION FOR SEQ ID NO: 67:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 120 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-153-67

Query Match 89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGSFSTYYTWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKPGESLRISCKGSGSFSTYYTWIGVWRQMPGKGLWNGIIPGDSDTY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYICTR-----GDRGVYWGQGLTVTVSS 116
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYICARWGSDGFYANDYWGQGLTVTVSS 120

RESULT 7
US-09-490-324-40
; Sequence 40, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:

/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)596-9000
/ TELEFAX: (212)596-9090
/ INFORMATION FOR SEQ ID NO: 67:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 120 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-324-40

Query Match 89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGSFSTYYTWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKPGESLRISCKGSGSFSTYYTWIGVWRQMPGKGLWNGIIPGDSDTY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYICTR-----GDRGVYWGQGLTVTVSS 116
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYICARWGSDGFYANDYWGQGLTVTVSS 120

RESULT 8
US-09-490-324-67
; Sequence 67, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-324-67

Query Match 89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 1e-48;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGSFSTYYTWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKPGESLRISCKGSGSFSTYYTWIGVWRQMPGKGLWNGIIPGDSDTY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYICTR-----GDRGVYWGQGLTVTVSS 116
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLSKASDTAMYICARWGSDGFYANDYWGQGLTVTVSS 120
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[illegible]

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; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; US-09-490-070A-26
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; Query Match 89.1%; Score 553.5; DB 2; Length 119;
; Best Local Similarity 89.9%; Pred. No. 1.9e-48;
; Matches 107; Conservative 2; Mismatches 7; Indels 3; Gaps 1;
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; QY 1 EVLVQSGAEVKKPGESLRISCKGSGDSFTYYIGWVRQMPGKLEWGIYPGDSDTIY 60
; DB 1 EVLVQSGAEVKKPGESLRISCKGSGVSFTSYIGWVRQMPGKLEWGIYPGDSDTRY 60
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; QY 61 SPSFQGVITISADKSI STAYLQWSSLKASDTAMYCYTR---GRRGVYWGQGLVTVYSS 116
; DB 61 SPSFQGVITISADKSI STAYLQWSSLKASDTAMYCARLGGGGYFDYWGQGLVTVYSS 119
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; RESULT 11
; US-09-490-153-26
; Sequence 26, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021

```

```

; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
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; US-09-490-070A-26
;
; Query Match 89.1%; Score 553.5; DB 2; Length 119;
; Best Local Similarity 89.9%; Pred. No. 1.9e-48;
; Matches 107; Conservative 2; Mismatches 7; Indels 3; Gaps 1;
;
; QY 1 EVLVQSGAEVKKPGESLRISCKGSGDSFTYYIGWVRQMPGKLEWGIYPGDSDTIY 60
; DB 1 EVLVQSGAEVKKPGESLRISCKGSGVSFTSYIGWVRQMPGKLEWGIYPGDSDTRY 60
;
; QY 61 SPSFQGVITISADKSI STAYLOWSSLKASDTAMYCYTR---GRRGVYWGQGLVTVYSS 116
; DB 61 SPSFQGVITISADKSI STAYLOWSSLKASDTAMYCARLGGGGYFDYWGQGLVTVYSS 119
;
; RESULT 11
; US-09-490-153-26
; Sequence 26, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 24-Jan-2000
APPLICATION NUMBER: US/09/490,153
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-153-26

Query Match 89.1%; Score 553.5; DB 2; Length 119;
Best Local Similarity 89.9%; Pred. No. 1.9e-48;
Matches 107; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSITY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSITY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCYCTR---GDRGVYWGQGLTVTVSS 116
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCYCARLGGGGYFYDWGQGLTVTVSS 119

RESULT 12
US-09-490-324-26
Sequence 26, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26

Query Match 89.1%; Score 553.5; DB 2; Length 119;
Best Local Similarity 89.9%; Pred. No. 1.9e-48;
Matches 107; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSITY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSITY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCYCTR---GDRGVYWGQGLTVTVSS 116
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCYCARLGGGGYFYDWGQGLTVTVSS 119

RESULT 13
US-09-920-262A-7
Sequence 7, Application US/09920262A
Patent No. 6902734
GENERAL INFORMATION:
APPLICANT: Shealy, David
Knight, David
APPLICANT: Scallion, Bernie
APPLICANT: Giles-Komar, Jill
APPLICANT: Peritt, David
TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CEN0248
CURRENT APPLICATION NUMBER: US/09/920,262A
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/223,358
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 60/236,827
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver 3.1
SEQ ID NO 7
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-09-920-262A-7

Query Match 81.4%; Score 505.5; DB 2; Length 119;
Best Local Similarity 80.7%; Pred. No. 1.3e-43;
Matches 96; Conservative 9; Mismatches 11; Indels 3; Gaps 1;

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Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCYCTR---GDRGVYWGQGLTVTVSS 116
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCYCARRRPGQGYFYDWGQGLTVTVSS 119

RESULT 14

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US-08-665-202-32
; Sequence 32, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-32

Query Match      80.0%; Score 496.5; DB 1; Length 129;
Best Local Similarity 72.9%; Pred. No. 1.1e-42;
Matches 94; Conservative 12; Mismatches 10; Indels 13; Gaps 1;

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Db      1 QVQLQSGAELKPKGESLRISCKGDSFTTWIGWVRQMPKGLGWGIIYPGDSDTIY 60
Qy      61 SPFGQGVTTISADKSIATYQLQWSLSKASDTAMYCYTRGDRG-----VDYWG 107
Db      61 SPFGQGVTTISVDKSVSTAYQLQWSLSKPSDSAVYFCARHDVGYCSSNCAKWPYFQHWG 120
Qy      108 QGTLVTSS 116
Db      121 QGTLVTSS 129

RESULT 15
US-09-315-574-32
; Sequence 32, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
```

```
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-315-574-32

Query Match      80.0%; Score 496.5; DB 2; Length 129;
Best Local Similarity 72.9%; Pred. No. 1.1e-42;
Matches 94; Conservative 12; Mismatches 10; Indels 13; Gaps 1;

Qy      1 EVQLVQSGAEVKKPGESLRISCKGDSFTTWIGWVRQMPKGLGWGIIYPGDSDTIY 60
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Qy      61 SPFGQGVTTISADKSIATYQLQWSLSKASDTAMYCYTRGDRG-----VDYWG 107
Db      61 SPFGQGVTTISVDKSVSTAYQLQWSLSKPSDSAVYFCARHDVGYCSSNCAKWPYFQHWG 120
Qy      108 QGTLVTSS 116
Db      121 QGTLVTSS 129

Search completed: December 3, 2005, 14:11:28
Job time : 50.2408 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:10:00 ; Search time 8.55102 Seconds
(without alignments)
256.916 Million cell updates/sec

Title: US-10-769-144-13

Perfect score: 33

Sequence: 1 TYWIG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	5	ADR46830	Adi46830 Human ant
2	33	100.0	5	ADR69905	Adi69905 Human IL-
3	33	100.0	5	ADY26777	Ady26777 Human ant
4	33	100.0	5	AEA18875	Aea18875 Amino aci
5	33	100.0	88	AAR22576	Aar22576 Heavy cha
6	33	100.0	109	ADI05782	Adi05782 Human mon
7	33	100.0	116	AAM48005	Aam48005 Human mon
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9	33	100.0	121	ADX02171	Adx02171 SARS coro
10	33	100.0	121	ADX02051	Adx02051 SARS coro
11	33	100.0	121	ADX02099	Adx02099 SARS coro
12	33	100.0	121	ADX02055	Adx02055 SARS coro
13	33	100.0	121	ADX02059	Adx02059 SARS coro
14	33	100.0	121	ADX02111	Adx02111 SARS coro
15	33	100.0	121	ADX02107	Adx02107 SARS coro
16	33	100.0	121	ADX02103	Adx02103 SARS coro
17	33	100.0	121	ADX02175	Adx02175 SARS coro
18	33	100.0	121	ADX02191	Adx02191 SARS coro
19	33	100.0	122	AAU02586	Aau02586 Anti-adip
20	33	100.0	125	ADY26764	Ady26764 Anti-NGF
21	33	100.0	130	ABP96715	Abp96715 Human ant
22	33	100.0	130	ADR69902	Adi69902 Human IL-
23	33	100.0	130	AEA18872	Aea18872 Amino aci
24	33	100.0	145	ABB65181	Abb65181 Drosophil

ALIGNMENTS

RESULT 1

ADR46830
ID ADR46830 standard; peptide; 5 AA.

XX AC ADR46830;

XX AC ADR46830;

DT 18-NOV-2004 (first entry)

XX DE Human antibody B11 heavy chain variable region CDR1 SEQ ID NO:13.

XX KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW betahCG; beta chorionic gonadotropin; antibody;
KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW antibody B11; heavy chain variable region; CDR;
KW complementarity determining region.

XX OS Homo sapiens.

OS XX WO2004074432-A2.

PD 02-SEP-2004.

XX PF 30-JAN-2004; 2004WO-US002725.

XX PR 31-JAN-2003; 2003US-0443979P.

XX PA (MEDA-) MEDAREX INC.

XX PI Keler T, Endres M, He L, Ramakrishna V;

XX DR WPI; 2004-635555/61.

XX PT New molecular conjugate having a monoclonal antibody that binds to human
APCs linked to a beta human chorionic gonadotropin, useful for inducing a
cytotoxic T cell response in cancers and infectious diseases.

XX PS Claim 9; SEQ ID NO 13; 82pp; English.

XX CC The present invention describes a molecular conjugate comprising a
monoclonal antibody that binds to human antigen presenting cells (APCs)
linked to beta human chorionic gonadotropin (betahCG), where the antibody
comprises a heavy and/or light chain variable region derived from a human
VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences

Abp43990 Human Bly
Adg94817 Single ch
Adx01988 SARS coro
Adx02018 SARS coro
Adx01958 SARS coro
Adx02020 SARS coro
Adx01960 SARS coro
Adx01962 SARS coro
Adx02028 SARS coro
Adx01984 SARS coro
Adx01986 SARS coro
Adx01982 SARS coro
Abu54587 Human NOV
Adr46829 Human p81
Ada34166 Acinetoba
Adr46819 Human ant
Adp64795 Nematode
Adr46827 Human bet
Adn21185 Bacterial
Adc24839 Human bre
Aab51824 Gene 47 h

25 33 100.0 248 5 ABP43990
26 33 100.0 248 7 ADG94817
27 33 100.0 253 9 ADX01988
28 33 100.0 254 9 ADX02018
29 33 100.0 254 9 ADX01958
30 33 100.0 254 9 ADX02020
31 33 100.0 254 9 ADX01960
32 33 100.0 254 9 ADX01962
33 33 100.0 254 9 ADX02028
34 33 100.0 254 9 ADX01984
35 33 100.0 255 9 ADX01986
36 33 100.0 255 9 ADX01982
37 33 100.0 373 6 ABUS4587
38 33 100.0 411 8 ADR46829
39 33 100.0 430 6 ADA34166
40 33 100.0 468 8 ADR46819
41 33 100.0 551 8 ADP64795
42 33 100.0 613 8 ADR46827
43 33 100.0 1627 8 ADN21185
44 32 97.0 78 7 ADC24839
45 32 97.0 116 3 AAB51824

of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to betahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents the human antibody B11 heavy chain variable region complementarity determining region 1 (CDR1) amino acid sequence, which is used in the exemplification of the present invention.

Sequence 5 AA;

Query Match 100.0%; Score 33; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
|
|
|
|
Db 1 TYWIG 5

RESULT 2

ADR69905
ID ADR69905 standard; peptide; 5 AA.

AC ADR69905;

DT 02-DEC-2004 (first entry)

XX Human IL-15 monoclonal antibody VH-region CDR1 SEQ ID NO:5.

XX monoclonal antibody; heavy chain variable region; interleukin-15; IL-15;
XX antiarthritic; ophthalmological; neuroprotective; nootropic;
KW gastrointestinal; hepatotropic; antiallergic; haemostatic;
KW dermatological; respiratory; cytostatic; immunosuppressive; vasotropic;
KW gynaecological; antimicrobial; CDR.

XX Homo sapiens.

XX WO2004076620-A2.

XX 10-SEP-2004.

XX 25-FEB-2004; 2004WO-IB000484.

XX 26-FEB-2003; 2003US-00374932.

PR 05-MAR-2003; 2003US-00379741.

XX (GENM-) GENMAB AS.

XX Van De Winkel JGJ, Van Dijk MA, Schuurman J, Gerritsen AF;
PI Baadsgaard OMS, Petersen J;
XX WPT; 2004-653391/63.

PT New isolated human monoclonal antibody that specifically binds to human
IL-15, useful for diagnosing, preventing or treating lupus, ulcerative
colitis, allograft rejection and graft-versus-host disease.

XX Claim 1; SEQ ID NO 5; 116pp; English.

XX The invention relates to a novel isolated human monoclonal antibody which
specifically binds to human interleukin-15 (IL-15) comprising at least
one CDR sequence from a fully defined sequence of 5, 17, 8, 12, 7 or 8
amino acids (ADR69905-ADR69910, respectively), a sequence at least 90,
95, 98 or 99% homologous to the amino acid sequences, or their fragments,
which retain the ability to specifically bind to human IL-15. A
monoclonal antibody of the invention has antiarthritic, ophthalmological,
neuroprotective, nootropic, gastrointestinal, hepatotropic, antiallergic,
haemostatic, dermatological, respiratory, cytostatic, immunosuppressive,
vasotropic, gynaecological, and antimicrobial activity. The methods and
compositions of the present invention are useful for the prevention
and/or treatment of conditions associated with aberrant expression or
activity of the IL-15, such as arthritis, connective tissue disorders,
ophthalmological disorders, neurological disorders, gastrointestinal and
hepatic disorders, allergic disorders, haematologic disorders, allergic
disorders, skin disorders, pulmonary disorders, malignancies,
transplantation-derived disorders, endocrinological disorders, vascular
disorders, gynaecological disorders and infectious diseases, including
ankylosing spondylitis, systemic lupus erythematosus, ulcerative colitis,
allograft rejection and graft-versus-host disease. The present sequence
represents CDR1 of the heavy chain variable (VH) region of a human IL-15
monoclonal antibody of the invention.

Sequence 5 AA;

Query Match 100.0%; Score 33; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
|
|
|
|
Db 1 TYWIG 5

RESULT 3

ADY26777

ID ADY26777 standard; protein; 5 AA.

AC ADY26777;

XX 19-MAY-2005 (first entry)

DT Human anti-NGF-antibody heavy chain CDR1 SEQ ID NO 92.

XX analgesic; gene therapy; antibody engineering; pharmaceutical; pain;
KW neurological disease; NGF; nerve growth factor; heavy chain; CDR1.

XX Homo sapiens.

XX WO2005019266-A2.

XX 03-MAR-2005.

XX 15-JUL-2004; 2004WO-US022876.

XX 15-JUL-2003; 2003US-0487431P.

XX (AMGE-) AMGEN INC.

XX Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;

XX


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PR 06-MAR-1991; 91GB-00004744.
PR 15-MAY-1991; 91GB-00010549.
PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA (MEDI-) MED RES COUNCIL.
XX
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD;
XX
XX WPI; 1992-056862/07.
DR
XX
XX Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic display
PT package.
XX
XX Disclosure; Page ?; 209pp; English.
XX
XX PCR was used to prepare a human scFv library from RNA from white blood
XX cells from an unimmunised donor. Heavy chains from IgG and IgM antibodies
XX were amplified separately. Four separate libraries were generated (IgG-K,
XX IgG-lambda, IgM-K and IgM-lambda). The purified scFv fragments were
XX ligated into the phagemid pHEX1 for expression on the surface of fd
XX bacteriophage as gene III fusions. The clones were then subjected to
XX affinity selection for binding to lysozyme by selection on tubes followed
XX by analysis by ELISA. 50 positive lysozyme binding clones were
XX identified, 95% being from the IgM library. The clones gave three
XX different BstNI restriction patterns, and at least 2 clones from each
XX pattern was sequenced. The sequences indicated the presence of 4 unique
XX human VH-VL combinations. The sequence shown here is one of the VH chains
XX found. See also AAR21260-307, 309-312, AAR22450, AAR22565, AAR22567-81
XX
XX Revised record issued on 23-SEP-2004 : Correction to sequence location
XX
XX Sequence 88 AA;
XX
XX Query Match 100.0%; Score 33; DB 2; Length 88;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TYWIG 5
XX |||||
XX 31 TYWIG 35
XX
XX
XX RESULT 6
XX ADI05782
XX ID ADI05782 standard; protein; 109 AA.
XX
XX AC ADI05782;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE Human monoclonal antibody CM-2 variable region heavy chain, SEQ ID 12.
XX
XX KW Cytostatic; Gene therapy; neoplasm; antibody; variable region;
XX heavy chain; proliferative disorder; human; CM-2.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Region 16..22
XX FT /label= CDR1
XX FT Region 40..47
XX FT /label= CDR2
XX FT Region 86..100
XX FT /label= CDR3
XX
XX PN WO2004005351-A2.
XX
XX PD 15-JAN-2004.
XX
XX PF 02-JUL-2003; 2003WO-IB003487.
XX

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PR 04-JUL-2002; 2002DE-01029906.
PR 04-JUL-2002; 2002DE-01029907.
PR 06-JUL-2002; 2002DE-01030516.
XX
XX (ONCO-) ONCOMAB GMBH.
XX
XX Mueller-Hermelink H, Vollmers H;
XX
XX WPI; 2004-122575/12.
DR N-PSDB; ADI05781.
XX
XX New purified polypeptide (e.g. an antibody) that induces apoptosis of a
PT neoplastic cell, useful for diagnosing or treating a neoplasm or a
PT proliferative disorder in mammals, including humans.
XX
XX Claim 93; SEQ ID NO 12; 106pp; English.
XX
XX The present invention relates to neoplasm specific antibody variable
XX region light and heavy chain sequences (ADI05771-ADI05782) The antibody
XX sequences are useful in diagnosing or treating a neoplasm or a
XX proliferative disorder in a mammal.
XX
XX Sequence 109 AA;
XX
XX Query Match 100.0%; Score 33; DB 8; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TYWIG 5
XX |||||
XX 20 TYWIG 24
XX
XX
XX RESULT 7
XX AAM48005
XX ID AAM48005 standard; protein; 116 AA.
XX
XX AC AAM48005;
XX
XX DT 08-MAR-2002 (first entry)
XX
XX DE Human monoclonal antibody B11 variable heavy chain protein.
XX
XX KW Human; monoclonal antibody; B11; antigen binding portion; dendritic cell;
XX mannose receptor; growth; cytolysis; pathogen; virus; bacterium;
XX autoimmune disease; inflammatory disorder; rheumatoid arthritis;
XX multiple sclerosis; diabetes mellitus; immunomodulatory;
XX antiinflammatory; antirheumatic; antiarthritic; neuroprotective;
XX antidiabetic; antianaemic; endocrine; dermatological; antithyroid;
XX uropathic; ophthalmological; muscular.
XX
XX OS Homo sapiens.
XX
XX PN WO200185798-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 08-MAY-2001; 2001WO-US015114.
XX
XX PR 08-MAY-2000; 2000US-0203126P.
XX 07-SEP-2000; 2000US-0230739P.
XX
XX (MEDA-) MEDAREX INC.
XX
XX Deo YM, Keler T;
XX
XX WPI; 2002-089788/12.
DR N-PSDB; ABA05500.
XX
XX New human monoclonal antibodies specific for dendritic cells, useful for
PT inhibiting growth or inducing cytolysis of a dendritic cell and treating
PT or preventing a dendritic cell mediated disease, e.g., autoimmune
PT disorders.
XX

```

XX PS Example 2; Fig 13; 95pp; English.

XX CC The invention relates to human monoclonal antibodies or their antigen

XX CC binding portions that specifically bind to dendritic cells and has one or

XX CC more of the following characteristics: (a) a binding affinity constant to

XX CC a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability

XX CC to opsonise a dendritic cell; (c) the ability to internalise after

XX CC binding to dendritic cells; or (d) the ability to activate dendritic

XX CC cells. The isolated human monoclonal antibody or its antigen binding

XX CC portion may also have any of the following characteristics: (a) mediates

XX CC cytolysis of dendritic cells in the presence of human effector cells; or

XX CC (b) inhibits growth of dendritic cells. The antibodies or its antigen

XX CC binding portion, binds to and blocks the human mannose receptor on

XX CC dendritic cells. The antibodies have immunomodulatory, antiinflammatory,

XX CC antirheumatic, antiarthritic, neuroprotective, antidiabetic, antianaemic,

XX CC endocrine, dermatological, antithyroid, uropathic, ophthalmological and

XX CC muscular activity. The antibodies or their antigen-binding fragments are

XX CC useful for inhibiting growth of a dendritic cell, inducing cytolysis of a

XX CC dendritic cell, treating or preventing a dendritic cell mediated disease,

XX CC detecting the presence of a dendritic cell, targeting an antigen to a

XX CC dendritic cell and preventing binding of a pathogen (a virus or a

XX CC bacterium) to human mannose receptor on dendritic cells. In particular,

XX CC the antibodies may be used to treat, autoimmune disease, graft versus

XX CC host disease, immune system or inflammatory disorders (e.g. rheumatoid

XX CC arthritis), multiple sclerosis, diabetes mellitus, myasthenia gravis,

XX CC pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's

XX CC syndrome and Graves disease. The present sequence is that of the human

XX CC monoclonal antibody B11 variable heavy chain, useful to the invention

XX SQ Sequence 116 AA;

Query Match 100.0%; Score 33; DB 5; Length 116;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TWIG 5
|||||

DB 31 TWIG 35

RESULT 8

ADR46821

ID ADR46821 standard; protein; 116 AA.

XX AC ADR46821;

XX DT 18-NOV-2004 (first entry)

XX DE Human antibody B11 heavy chain variable region protein SEQ ID NO:4.

XX KW molecular conjugate; monoclonal antibody; human antigen presenting cell;

XX KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;

XX KW betaHCG; beta chorionic gonadotropin; antibody;

XX KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;

XX KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;

XX KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;

XX KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;

XX KW antibody B11; heavy chain variable region.

XX OS Homo sapiens.

XX PN WO2004074432-A2.

XX PD 02-SEP-2004.

XX PF 30-JAN-2004; 2004WO-US0002725.

XX PR 31-JAN-2003; 2003US-0443979P.

XX PA (MEDA-) MEDAREX INC.

XX PI Keler T, Endres M, He L, Ramakrishna V;

XX WPI; 2004-635555/61.

XX N-PSDB; ADR46820.

XX PT New molecular conjugate having a monoclonal antibody that binds to human

XX PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a

XX PT cytotoxic T cell response in cancers and infectious diseases.

XX PS Claim 11; SEQ ID NO 4; 82pp; English.

XX CC The present invention describes a molecular conjugate comprising a

XX CC monoclonal antibody that binds to human antigen presenting cells (APCs)

XX CC linked to beta human chorionic gonadotropin (betaHCG), where the antibody

XX CC comprises a heavy and/or light chain variable region derived from a human

XX CC VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences

XX CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also

XX CC described: (1) a molecular conjugate comprising a human antibody heavy

XX CC chain and a human antibody light chain, where either or both chains are

XX CC linked to betaHCG; (2) a molecular conjugate comprising a human single

XX CC chain antibody that binds to human APCs linked to betaHCG, where the

XX CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12

XX CC (ADR46829); (3) a composition comprising any of the molecular conjugates

XX CC as described above, and a carrier, optionally in combination with an

XX CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,

XX CC against betaHCG, comprising contacting any of the molecular conjugates

XX CC described above with APCs such that the antigen is processed and

XX CC presented to T cells in a manner which induces or enhances a T cell-

XX CC mediated response against the antigen; (5) immunising a subject

XX CC comprising administering any of the molecular conjugates described above,

XX CC optionally in combination with an adjuvant, a cytokine which stimulates

XX CC proliferation of dendritic cells and/or an immunostimulatory agent; and

XX CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,

XX CC comprising forming a conjugate of the antigen and a monoclonal antibody

XX CC which binds to APCs, and contacting the conjugate either in vivo or ex

XX CC vivo with APCs such that the antigen is internalised, processed and

XX CC presented to T cells in a manner which induces or enhances a cytotoxic T

XX CC cell response against the antigen. The molecular conjugate has

XX CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,

XX CC virucide and antimalarial activities, and can be used as a CD8 agonist,

XX CC and in vaccines. The methods and compositions of the present invention

XX CC are useful for inducing a cytotoxic T cell response, and in particular

XX CC for treating autoimmune disorders, cancers and infectious diseases by

XX CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,

XX CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and

XX CC herpes. The present sequence represents a human antibody B11 heavy chain

XX CC variable region, which is used in the exemplification of the present

XX CC invention.

XX SQ Sequence 116 AA;

Query Match 100.0%; Score 33; DB 8; Length 116;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TWIG 5
|||||

DB 31 TWIG 35

RESULT 9

ADX02171

ID ADX02171 standard; protein; 121 AA.

XX AC ADX02171;

XX DT 21-APR-2005 (first entry)

XX DE SARS coronavirus antibody heavy chain SEQ ID NO 427.

XX KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;

XX KW respiratory disease; infection; antibody; heavy chain.

XX OS SARS coronavirus.

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XX WO2005012360-A2.
XX 10-FEB-2005.
XX
XX 21-JUL-2004; 2004WO-EP051568.
XX
XX 22-JUL-2003; 2003WO-EP050328.
XX 01-SEP-2003; 2003WO-EP050391.
XX 16-OCT-2003; 2003WO-EP050723.
XX 24-NOV-2003; 2003WO-EP050883.
XX 04-DEC-2003; 2003WO-EP050943.
XX 02-FEB-2004; 2004WO-EP050067.
XX 13-FEB-2004; 2004WO-EP050127.
XX 19-MAR-2004; 2004WO-EP050334.
XX 07-APR-2004; 2004WO-EP050464.
XX 14-APR-2004; 2004WO-EP050516.
XX 29-APR-2004; 2004WO-EP050643.
XX
XX (CRUC-) CRUCELL HOLLAND BV.
XX
XX Ter Meulen JH, De Kruij CA, Van Den Brink EN, Goudemits J;
XX N-PSDB; ADX02170.
XX
XX WPI; 2005-142879/15.
XX
XX New binding molecules that specifically bind to severe acute respiratory
XX syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
XX treating conditions resulting from SARS-CoV.
XX
XX Claim 4; SEQ ID NO 427; 633pp; English.
XX
XX The invention relates to a binding molecule, or its variant, capable of
XX specifically binding to a severe acute respiratory syndrome (SARS)-
XX coronavirus (CoV). The composition (including the binding molecule or its
XX functional variant, or the immunoconjugate) is useful as a medicament for
XX the diagnosis, prophylaxis or treatment of a condition resulting from a
XX SARS-CoV, or in the preparation of the medicament. The present sequence
XX represents a SARS coronavirus binding molecule heavy chain.
XX
XX Sequence 121 AA;
XX
XX Query Match 100.0%; Score 33; DB 9; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 TYWIG 5
XX |||||
XX 33 TYWIG 37
XX
XX Db
XX
XX RESULT 10
XX ID ADX02051 standard; protein; 121 AA.
XX
XX AC ADX02051;
XX
XX 21-APR-2005 (first entry)
XX
XX SARS coronavirus antibody heavy chain SEQ ID NO 307.
XX
XX severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
XX respiratory disease; infection; antibody; heavy chain.
XX
XX SARS coronavirus.
XX
XX WO2005012360-A2.
XX
XX 10-FEB-2005.
XX
XX 21-JUL-2004; 2004WO-EP051568.
XX
XX 22-JUL-2003; 2003WO-EP050328.
XX 01-SEP-2003; 2003WO-EP050391.
XX 16-OCT-2003; 2003WO-EP050723.
XX 24-NOV-2003; 2003WO-EP050883.
XX 04-DEC-2003; 2003WO-EP050943.
XX 02-FEB-2004; 2004WO-EP050067.
XX 13-FEB-2004; 2004WO-EP050127.
XX 19-MAR-2004; 2004WO-EP050334.
XX 07-APR-2004; 2004WO-EP050464.
XX 14-APR-2004; 2004WO-EP050516.
XX 29-APR-2004; 2004WO-EP050643.
XX
XX (CRUC-) CRUCELL HOLLAND BV.
XX
XX Ter Meulen JH, De Kruij CA, Van Den Brink EN, Goudemits J;
XX N-PSDB; ADX02170.
XX
XX WPI; 2005-142879/15.
XX
XX New binding molecules that specifically bind to severe acute respiratory
XX syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
XX treating conditions resulting from SARS-CoV.
XX
XX Claim 4; SEQ ID NO 427; 633pp; English.
XX
XX The invention relates to a binding molecule, or its variant, capable of
XX specifically binding to a severe acute respiratory syndrome (SARS)-
XX coronavirus (CoV). The composition (including the binding molecule or its
XX functional variant, or the immunoconjugate) is useful as a medicament for
XX the diagnosis, prophylaxis or treatment of a condition resulting from a
XX SARS-CoV, or in the preparation of the medicament. The present sequence
XX represents a SARS coronavirus binding molecule heavy chain.
XX
XX Sequence 121 AA;
XX
XX Query Match 100.0%; Score 33; DB 9; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 TYWIG 5
XX |||||
XX 33 TYWIG 37
XX
XX Db
XX
XX RESULT 10
XX ID ADX02051 standard; protein; 121 AA.
XX
XX AC ADX02051;
XX
XX 21-APR-2005 (first entry)
XX
XX SARS coronavirus antibody heavy chain SEQ ID NO 307.
XX
XX severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
XX respiratory disease; infection; antibody; heavy chain.
XX
XX SARS coronavirus.
XX
XX WO2005012360-A2.
XX
XX 10-FEB-2005.
XX
XX 21-JUL-2004; 2004WO-EP051568.
XX
XX 22-JUL-2003; 2003WO-EP050328.

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PR 01-SEP-2003; 2003WO-EP050391.
PR 16-OCT-2003; 2003WO-EP050723.
PR 24-NOV-2003; 2003WO-EP050883.
PR 04-DEC-2003; 2003WO-EP050943.
PR 02-FEB-2004; 2004WO-EP050067.
PR 13-FEB-2004; 2004WO-EP050127.
PR 19-MAR-2004; 2004WO-EP050334.
PR 07-APR-2004; 2004WO-EP050464.
PR 14-APR-2004; 2004WO-EP050516.
PR 29-APR-2004; 2004WO-EP050643.
XX
XX (CRUC-) CRUCELL HOLLAND BV.
XX
XX Ter Meulen JH, De Kruij CA, Van Den Brink EN, Goudemits J;
XX N-PSDB; ADX02050.
XX
XX WPI; 2005-142879/15.
XX
XX New binding molecules that specifically bind to severe acute respiratory
XX syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
XX treating conditions resulting from SARS-CoV.
XX
XX Claim 4; SEQ ID NO 307; 633pp; English.
XX
XX The invention relates to a binding molecule, or its variant, capable of
XX specifically binding to a severe acute respiratory syndrome (SARS)-
XX coronavirus (CoV). The composition (including the binding molecule or its
XX functional variant, or the immunoconjugate) is useful as a medicament for
XX the diagnosis, prophylaxis or treatment of a condition resulting from a
XX SARS-CoV, or in the preparation of the medicament. The present sequence
XX represents a SARS coronavirus binding molecule heavy chain.
XX
XX Sequence 121 AA;
XX
XX Query Match 100.0%; Score 33; DB 9; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 TYWIG 5
XX |||||
XX 33 TYWIG 37
XX
XX Db
XX
XX RESULT 11
XX ID ADX02099 standard; protein; 121 AA.
XX
XX AC ADX02099;
XX
XX 21-APR-2005 (first entry)
XX
XX SARS coronavirus antibody heavy chain SEQ ID NO 355.
XX
XX severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
XX respiratory disease; infection; antibody; heavy chain.
XX
XX SARS coronavirus.
XX
XX WO2005012360-A2.
XX
XX 10-FEB-2005.
XX
XX 21-JUL-2004; 2004WO-EP051568.
XX
XX 22-JUL-2003; 2003WO-EP050328.
XX 01-SEP-2003; 2003WO-EP050391.
XX 16-OCT-2003; 2003WO-EP050723.
XX 24-NOV-2003; 2003WO-EP050883.
XX 04-DEC-2003; 2003WO-EP050943.
XX 02-FEB-2004; 2004WO-EP050067.
XX 13-FEB-2004; 2004WO-EP050127.
XX 19-MAR-2004; 2004WO-EP050334.
XX 07-APR-2004; 2004WO-EP050464.

```

PR 14-APR-2004; 2004WO-EP050516.
PR 29-APR-2004; 2004WO-EP050643.
PA (CRUC-) CRUCELL HOLLAND BV.
XX Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudemits J;
XX N-PSDB; ADX02098.
DR WPI; 2005-142879/15.
XX N-PSDB; ADX02098.
PT New binding molecules that specifically bind to severe acute respiratory
PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
PT treating conditions resulting from SARS-CoV.
XX Claim 4; SEQ ID NO 355; 633pp; English.
XX The invention relates to a binding molecule, or its variant, capable of
CC specifically binding to a severe acute respiratory syndrome (SARS)-
CC coronavirus (CoV). The composition (including the binding molecule or its
CC functional variant, or the immunoconjugate) is useful as a medicament for
CC the diagnosis, prophylaxis or treatment of a condition resulting from a
CC SARS-CoV, or in the preparation of the medicament. The present sequence
CC represents a SARS coronavirus binding molecule heavy chain.
XX SQ Sequence 121 AA;
SQ Query Match 100.0%; Score 33; DB 9; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYWIG 5
Db |||||
33 TYWIG 37
RESULT 12
ADX02055
ID ADX02055 standard; protein; 121 AA.
AC ADX02055;
XX 21-APR-2005. (first entry)
XX SARS coronavirus antibody heavy chain SEQ ID NO 311.
DE severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
KW respiratory disease; infection; antibody; heavy chain.
XX SARS coronavirus.
XX WO2005012360-A2.
XX 10-FEB-2005.
XX 21-JUL-2004; 2004WO-EP051568.
XX 22-JUL-2003; 2003WO-EP050328.
PR 01-SEP-2003; 2003WO-EP050391.
PR 16-OCT-2003; 2003WO-EP050723.
PR 24-NOV-2003; 2003WO-EP050883.
PR 04-DEC-2003; 2003WO-EP050943.
PR 02-FEB-2004; 2004WO-EP050067.
PR 13-FEB-2004; 2004WO-EP050127.
PR 19-MAR-2004; 2004WO-EP050334.
PR 07-APR-2004; 2004WO-EP050464.
PR 14-APR-2004; 2004WO-EP050516.
PR 29-APR-2004; 2004WO-EP050643.
XX (CRUC-) CRUCELL HOLLAND BV.
PA Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudemits J;
XX WPI; 2005-142879/15.
XX N-PSDB; ADX02058.

DR N-PSDB; ADX02054.
XX New binding molecules that specifically bind to severe acute respiratory
PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
PT treating conditions resulting from SARS-CoV.
XX Claim 4; SEQ ID NO 311; 633pp; English.
XX The invention relates to a binding molecule, or its variant, capable of
CC specifically binding to a severe acute respiratory syndrome (SARS)-
CC coronavirus (CoV). The composition (including the binding molecule or its
CC functional variant, or the immunoconjugate) is useful as a medicament for
CC the diagnosis, prophylaxis or treatment of a condition resulting from a
CC SARS-CoV, or in the preparation of the medicament. The present sequence
CC represents a SARS coronavirus binding molecule heavy chain.
XX SQ Sequence 121 AA;
SQ Query Match 100.0%; Score 33; DB 9; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYWIG 5
Db |||||
33 TYWIG 37
RESULT 13
ADX02059
ID ADX02059 standard; protein; 121 AA.
AC ADX02059;
XX 21-APR-2005 (first entry)
XX SARS coronavirus antibody heavy chain SEQ ID NO 315.
DE severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
KW respiratory disease; infection; antibody; heavy chain.
XX SARS coronavirus.
XX WO2005012360-A2.
XX 10-FEB-2005.
XX 21-JUL-2004; 2004WO-EP051568.
XX 22-JUL-2003; 2003WO-EP050328.
PR 01-SEP-2003; 2003WO-EP050391.
PR 16-OCT-2003; 2003WO-EP050723.
PR 24-NOV-2003; 2003WO-EP050883.
PR 04-DEC-2003; 2003WO-EP050943.
PR 02-FEB-2004; 2004WO-EP050067.
PR 13-FEB-2004; 2004WO-EP050127.
PR 19-MAR-2004; 2004WO-EP050334.
PR 07-APR-2004; 2004WO-EP050464.
PR 14-APR-2004; 2004WO-EP050516.
PR 29-APR-2004; 2004WO-EP050643.
XX (CRUC-) CRUCELL HOLLAND BV.
PA Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudemits J;
XX WPI; 2005-142879/15.
XX N-PSDB; ADX02058.
XX New binding molecules that specifically bind to severe acute respiratory
PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
PT treating conditions resulting from SARS-CoV.
XX Claim 4; SEQ ID NO 315; 633pp; English.
XX

CC The invention relates to a binding molecule, or its variant, capable of
 CC specifically binding to a severe acute respiratory syndrome (SARS)-
 CC coronavirus (Cov). The composition (including the binding molecule or its
 CC functional variant, or the immunoconjugate) is useful as a medicament for
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a
 CC SARS-CoV, or in the preparation of the medicament. The present sequence
 CC represents a SARS coronavirus binding molecule heavy chain.

xx SQ Sequence 121 AA;

Query Match 100.0%; Score 33; DB 9; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
 |||||
 Db 33 TYWIG 37

RESULT 14
 ADX02111
 ID ADX02111 standard; protein; 121 AA.

xx AC ADX02111;
 xx DT 21-APR-2005 (first entry)

xx DE SARS coronavirus antibody heavy chain SEQ ID NO 367.

xx KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 xx respiratory disease; infection; antibody; heavy chain.

xx OS SARS coronavirus.
 xx PN WO2005012360-A2.

xx PD 10-FEB-2005.

xx PF 21-JUL-2004; 2004WO-EP051568.

xx PR 22-JUL-2003; 2003WO-EP050328.

xx PR 01-SEP-2003; 2003WO-EP050391.

xx PR 16-OCT-2003; 2003WO-EP050723.

xx PR 24-NOV-2003; 2003WO-EP050883.

xx PR 04-DEC-2003; 2003WO-EP050943.

xx PR 02-FEB-2004; 2004WO-EP050067.

xx PR 13-FEB-2004; 2004WO-EP050127.

xx PR 19-MAR-2004; 2004WO-EP050334.

xx PR 07-APR-2004; 2004WO-EP050464.

xx PR 14-APR-2004; 2004WO-EP050516.

xx PR 29-APR-2004; 2004WO-EP050643.

xx PA (CRUC-) CRUCELL HOLLAND BV.

xx PI Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudamit J;

xx DR WPI; 2005-142879/15.

xx DR N-PSDB; ADX02110.

xx PT New binding molecules that specifically bind to severe acute respiratory
 xx syndrome (SARS)-coronavirus (Cov), useful for diagnosing, preventing or
 xx treating conditions resulting from SARS-CoV.

xx PS Claim 4; SEQ ID NO 367; 633pp; English.

xx CC The invention relates to a binding molecule, or its variant, capable of
 xx specifically binding to a severe acute respiratory syndrome (SARS)-
 xx coronavirus (Cov). The composition (including the binding molecule or its
 xx functional variant, or the immunoconjugate) is useful as a medicament for
 xx the diagnosis, prophylaxis or treatment of a condition resulting from a
 xx SARS-CoV, or in the preparation of the medicament. The present sequence
 xx represents a SARS coronavirus binding molecule heavy chain.

SQ Sequence 121 AA;

Query Match 100.0%; Score 33; DB 9; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
 |||||
 Db 33 TYWIG 37

RESULT 15
 ADX02107
 ID ADX02107 standard; protein; 121 AA.

xx AC ADX02107;

xx DT 21-APR-2005 (first entry)

xx DE SARS coronavirus antibody heavy chain SEQ ID NO 363.

xx KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 xx respiratory disease; infection; antibody; heavy chain.

xx OS SARS coronavirus.

xx PN WO2005012360-A2.

xx PD 10-FEB-2005.

xx PF 21-JUL-2004; 2004WO-EP051568.

xx PR 22-JUL-2003; 2003WO-EP050328.

xx PR 01-SEP-2003; 2003WO-EP050391.

xx PR 16-OCT-2003; 2003WO-EP050723.

xx PR 24-NOV-2003; 2003WO-EP050883.

xx PR 04-DEC-2003; 2003WO-EP050943.

xx PR 02-FEB-2004; 2004WO-EP050067.

xx PR 13-FEB-2004; 2004WO-EP050127.

xx PR 19-MAR-2004; 2004WO-EP050334.

xx PR 07-APR-2004; 2004WO-EP050464.

xx PR 14-APR-2004; 2004WO-EP050516.

xx PR 29-APR-2004; 2004WO-EP050643.

xx PA (CRUC-) CRUCELL HOLLAND BV.

xx PI Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudamit J;
 xx WPI; 2005-142879/15.

xx DR N-PSDB; ADX02106.

xx PT New binding molecules that specifically bind to severe acute respiratory
 xx syndrome (SARS)-coronavirus (Cov), useful for diagnosing, preventing or
 xx treating conditions resulting from SARS-CoV.

xx PS Claim 4; SEQ ID NO 363; 633pp; English.

xx CC The invention relates to a binding molecule, or its variant, capable of
 xx specifically binding to a severe acute respiratory syndrome (SARS)-
 xx coronavirus (Cov). The composition (including the binding molecule or its
 xx functional variant, or the immunoconjugate) is useful as a medicament for
 xx the diagnosis, prophylaxis or treatment of a condition resulting from a
 xx SARS-CoV, or in the preparation of the medicament. The present sequence
 xx represents a SARS coronavirus binding molecule heavy chain.

SQ Sequence 121 AA;
 Query Match 100.0%; Score 33; DB 9; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
 |||||

Db 33 TYWIG 37

Search completed: December 3, 2005, 14:25:04
Job time : 9.55102 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:59 ; Search time 1.36735 Seconds
(without alignments)
351.837 Million cell updates/sec

Title: US-10-769-144-13

Perfect score: 33

Sequence: 1 TYWIG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	98	2 PH0877	Ig heavy chain V r
2	33	100.0	102	2 PH1260	Ig heavy chain V r
3	33	100.0	102	2 PH1263	Ig heavy chain V r
4	33	100.0	117	2 S19669	Ig heavy chain V r
5	33	100.0	119	2 S36257	Ig heavy chain V r
6	33	100.0	123	2 PH1413	Ig heavy chain V r
7	33	100.0	127	2 PH1409	Ig heavy chain V r
8	33	100.0	175	2 S57903	probable amino aci
9	33	100.0	181	2 F75561	hypothetical prote
10	33	100.0	324	2 E84505	hypothetical prote
11	33	100.0	332	2 E71105	hypothetical prote
12	33	100.0	333	2 G75055	hypothetical prote
13	33	100.0	348	2 E82896	hemin permease U03
14	33	100.0	390	2 D82186	beta-lactamase-rel
15	33	100.0	466	2 A95963	probable oxidoredu
16	33	100.0	539	2 S30871	hypothetical prote
17	33	100.0	539	2 A88546	protein R107.1 (im
18	33	100.0	1562	2 T43022	ATP-binding multidi
19	32	97.0	156	2 S67248	hypothetical prote
20	32	97.0	281	2 S55646	hypothetical prote
21	32	97.0	294	2 AC1905	ABC transporter su
22	32	97.0	387	2 T22841	hypothetical prote
23	32	97.0	528	2 S50563	hypothetical prote
24	32	97.0	533	1 GR8YCP	cytosine/purine tr
25	32	97.0	760	2 E81808	hypothetical prote
26	32	97.0	881	2 E87387	TonB-dependent rec
27	32	97.0	1077	2 D90387	peptidase related
28	32	97.0	1118	1 A49724	protein-tyrosine-p
29	31	93.9	69	2 AB1333	hypothetical prote

ALIGNMENTS

RESULT 1

PH0877

Ig heavy chain V region (anti-DNA, II-1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996

C:Accession: PH0877

R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Grossein, C.; Smith, A.; Diamond, B.

J. Exp. Med. 174, 1639-1652, 1991

A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype

A:Reference number: PH0862; MUID:92078875; PMID:1660528

A:Accession: PH0877

A:Molecule type: DNA

A:Residues: 1-98 <MAN>

A:Cross-references: UNIPARC:UPI0000176C1P

C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:50-66/Region: complementarity-determining 2

Query Match 100.0%; Score 33; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5

DB 31 TYWIG 35

RESULT 2

PH1260

Ig heavy chain V region (clone CD-4) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1260

R:Cal, J.; Humphries, C.; Richardson, A.; Tucker, P.W.

J. Exp. Med. 176, 1073-1081, 1992

A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron

A:Reference number: PH1232; MUID:93018822; PMID:1402653

A:Accession: PH1260

A:Molecule type: DNA

A:Residues: 1-102 <CAI>

A:Cross-references: UNIPARC:UPI0000176SCF

A:Experimental source: cord blood B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

hypothetical prote
30S ribosomal prot
protein export mem
probable nIKC prot
ABC transporter, m
conserved hypotHet
hypothetical prote
hypothetical prote
hypothetical prote
NADH2 dehydrogenas
conserved hypotHet
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r

30 31 93.9 69 2 AB1704
31 31 93.9 83 2 E83178
32 31 93.9 100 1 F70309
33 31 93.9 301 2 H97505
34 31 93.9 301 2 AD2724
35 31 93.9 372 2 T42426
36 31 93.9 384 2 G84482
37 31 93.9 384 2 T49128
38 31 93.9 535 2 E87656
39 31 93.9 641 2 S63645
40 29 87.9 78 2 F69790
41 29 87.9 86 2 S12580
42 29 87.9 98 2 PH1274
43 29 87.9 98 2 S26907
44 29 87.9 101 2 S12428
45 29 87.9 101 2 S12424

Qy 1 TYWIG 5
|||||
Db 35 TYWIG 39

RESULT 3
PH1263
Ig heavy chain V region (clone VERG2) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1263
R:Caiz, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chronic lymphocytic leukemia
A:Reference number: PH1232; MUID:93018622; PMID:1402653
A:Accession: PH1263
A:Molecule type: mRNA
A:Residues: 1-102 <CAI>
A:Cross-references: UNIPARC:UPI0000176BD0
A:Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 28; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

Qy 1 TYWIG 5
|||||
Db 35 TYWIG 39

RESULT 4
S19669
Ig heavy chain V region (VH5DJ) - human
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19669
R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A:Title: BY-passing immunization. Human antibodies from V-gene libraries displayed on phage
A:Reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19669
A:Molecule type: mRNA
A:Residues: 1-117 <MAR>
A:Cross-references: UNIPARC:UPI0000115FEA; EMBL:X61651; NID:g37731; PIDN:CAA43832.1; PIDN:CAA43832.1; PIDN:CAA43832.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 32; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

Qy 1 TYWIG 5
|||||
Db 31 TYWIG 35

RESULT 5
S36257
Ig heavy chain V region (clone alpha-CD4-74) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36257
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36257
A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-119 <GRI>
A:Cross-references: UNIPARC:UPI0000118DE9; EMBL:Z18848; NID:g33122; PIDN:CAA79300.1; PIDN:CAA79300.1; PIDN:CAA79300.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 33; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

Qy 1 TYWIG 5
|||||
Db 31 TYWIG 35

RESULT 6
PH1413
Ig heavy chain V region (clone P1-56) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: PH1413
R:van der Stoep, N.; van der Linden, J.; Logtenberg, T. J. Exp. Med. 177, 99-107, 1993
A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of somatic mutations
A:Reference number: PH1409; MUID:93115676; PMID:8418213
A:Accession: PH1413
A:Molecule type: mRNA
A:Residues: 1-123 <VAN>
A:Cross-references: UNIPARC:UPI0000176A34
A:Experimental source: PBMC
A>Note: the authors translated the codon CTG for residue 115 as Met
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 34; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

Qy 1 TYWIG 5
|||||
Db 31 TYWIG 35

RESULT 7
PH1409
Ig heavy chain V region (clone P1-51) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1409
R:van der Stoep, N.; van der Linden, J.; Logtenberg, T. J. Exp. Med. 177, 99-107, 1993
A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of somatic mutations
A:Reference number: PH1409; MUID:93115676; PMID:8418213
A:Accession: PH1409
A:Molecule type: mRNA
A:Residues: 1-127 <VAN>
A:Cross-references: UNIPARC:UPI0000176B99
A:Experimental source: PBMC
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 35; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

Qy 1 TYWIG 5
|||||
Db 31 TYWIG 35

A;Accession: E84505
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <STO>
A;Cross-references: UNIPROT:Q9SL55; UNIPARC:UPI00000A669E; GB:AE002093; NID:G945
C;Genetics:
A;Gene: At2g13130
A;Map position: 2
C;Superfamily: hypothetical protein containing F-box domain

Query Match 100.0%; Score 33; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 TYWIG 5
Db 129 TYWIG 133

RESULT 11
E71105
hypothetical protein PH0614 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: E71105
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic bacterium
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: E71105
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-332 <KAW>
A;Cross-references: UNIPROT:O58348; UNIPARC:UPI0000139B2F; GB:AP000003; NID:G521
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by
C;Genetics:
A;Gene: PH0614

Query Match 100.0%; Score 33; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 TYWIG 5
Db 204 TYWIG 208

RESULT 12
G75055
hypothetical protein PAB0953 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C;Accession: G75055
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromatin
A;Reference number: A75001
A;Accession: G75055
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-333 <KAW>
A;Cross-references: UNIPROT:Q9UY52; UNIPARC:UPI0000139B6C; GB:AJ248287; GB:AL08
C;Genetics:
A;Gene: PAB0953
C;Superfamily: hypothetical protein PYRAB14350 precursor

Query Match 100.0%; Score 33; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

QY      1 TYWIG 5
      |||||
Db      204 TYWIG 208

RESULT 13
hemin permease U0399 [imported] - Ureaplasma urealyticum
C/Species: Ureaplasma urealyticum
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: E82896
R/Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A/Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A/Reference number: A82870
A/Accession: E82896
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-348 <GLA>
A/Cross-references: UNIPARC:UPI00000C1C54; GB:AF222894; NID:G6899377; PIDN:
A/Experimental source: serovar 3; biovar 1
C/Genetics:
A/Gene: hmuU-2; U0399
A/Genetic code: SGC3

Query Match      100.0%; Score 33; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYWIG 5
      |||||
Db      314 TYWIG 318

RESULT 14
beta-lactamase-related protein VC1562 [imported] - Vibrio cholerae (strain N16961 serogr
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: D82186
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, B
1. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: D82186
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-390 <HEI>
A/Cross-references: UNIPROT:Q9KRS4; UNIPARC:UPI00000C301A; GB:AE004233; GB:AE003852; NID
A/Experimental source: serogroup O1, strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC1562
A/Map position: 1

Query Match      100.0%; Score 33; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYWIG 5
      |||||
Db      100 TYWIG 104

RESULT 15
A95963
probable oxidoreductase protein tauD [imported] - Sinorhizobium meliloti (strain 1021) m
C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C/Accession: A95963
R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

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A/Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
A/Reference number: A95842; MUID:21396508; PMID:111481431
A/Accession: A95963
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-466 <KUR>
A/Cross-references: UNIPROT:Q92UW7; UNIPARC:UPI00000CB6FC; GB:AL591985; PIDN:CAC49369.1;
A/Experimental source: strain 1021, megaplasmid pSymB
R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A/Reference number: A96039; MUID:21368234; PMID:11474104
A/Contents: annotation
C/Genetics:
A/Gene: tauD; SMB21529
A/Genome: plasmid

Query Match      100.0%; Score 33; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYWIG 5
      |||||
Db      36 TYWIG 40

Search completed: December 3, 2005, 14:33:34
Job time : 3.36735 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:48 ; Search time 8.81633 Seconds
(without alignments)
400.126 Million cell updates/sec

Title: US-10-769-144-13
Perfect score: 33
Sequence: 1 TYWIG 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	103	2	Q81Q53 DROME
2	33	100.0	137	2	Q81GH9 DROSOPHILA
3	33	100.0	145	2	Q9VRL1 DROSOPHILA
4	33	100.0	145	2	Q6X125 DROXYA
5	33	100.0	150	2	Q8W1A2 ORYSA
6	33	100.0	166	2	Q9UDK8 HUMAN
7	33	100.0	175	1	YPEV LACDL
8	33	100.0	178	2	Q4MRV1 BACCE
9	33	100.0	178	2	Q6HDH2 BACHK
10	33	100.0	178	2	Q73014 BACCL1
11	33	100.0	178	2	Q81B88 BACCR
12	33	100.0	178	2	Q81LN5 BACAN
13	33	100.0	178	2	Q634J1 BACCZ
14	33	100.0	181	2	Q9RY56 DEIRA
15	33	100.0	189	2	Q8C634 MOUSE
16	33	100.0	192	2	Q9ND13 ENTHI
17	33	100.0	192	2	Q511T9 ENTHI
18	33	100.0	192	2	Q4QT07 ENTHI
19	33	100.0	192	2	Q5EGP4 ENTHI
20	33	100.0	250	2	Q84JP6 ARATH
21	33	100.0	256	2	Q8TDP9 HUMAN
22	33	100.0	268	2	Q8W189 ORYSA
23	33	100.0	281	2	Q75XR6 HORSE
24	33	100.0	303	2	Q67SS6 SYNTH
25	33	100.0	324	2	Q9SL55 ARATH
26	33	100.0	332	1	Y614 PYRHO
27	33	100.0	333	1	Y1435 PYRAB
28	33	100.0	333	2	Q8U3H9 PYRFU
29	33	100.0	341	2	Q554Z3 DICI1
30	33	100.0	348	2	Q9PQ91 UREPA
31	33	100.0	360	2	Q4FQL5_9GAMM

Q8Y009 ralstonia s
Q8D429 vibrio vuln
Q9KR94 vibrio chol
Q7mfk0 vibrio vuln
Q617d4 caenorhabdi
Q88sq8 lactobacill
Q8rh44 paracoccus
Q8rh53 paracoccus
Q6rh61 paracoccus
Q92uw7 rhizobium m
Q7nd75 gloeobacter
P32739 caenorhabdi
Q7nkz5 gloeobacter
Q4li93 gibberella

ALIGNMENTS

RESULT 1

Q81Q53 DROME PRELIMINARY; PRT; 103 AA.
AC Q81Q53;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG10640-PB, isoform B.
GN Name=Dv1A; ORFNames=CG10640;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA ADAMS M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Huston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."

```
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bargman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Minkler J.S., Millburn G.H., Prochownik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
DR EMBL; AE003566; AAN12119.1; -; Genomic_DNA.
DR HSPF; Q15819; 1J7D.
DR Ensemble; CG10640; Drosophila melanogaster.
DR FlyBase; FBgn0035601; Uevia.
DR FlyBase; FBgn0035601; Uevia.
DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR000608; UBO-conjugat_E2.
DR Pfam; PF00179; UQ con; 1.
DR ProDom; PD000463; UBO_conjugat; 1.
DR SMART; SM00212; UBCC; 1.
DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
FT NON TER 1
SQ SEQUENCE 103 AA; 12165 MW; 8569382F12E36F7E CRC64;

Query Match 100.0%; Score 33; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYWIG 5
DB 4 TYWIG 8

RESULT 2
O8IGH9 DROME
ID O8IGH9_DROME PRELIMINARY; PRT; 137 AA.

Query Match 100.0%; Score 33; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYWIG 5
DB 4 TYWIG 8

RESULT 3
O9VRL1 DROME
ID O9VRL1_DROME PRELIMINARY; PRT; 145 AA.

Query Match 100.0%; Score 33; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. NO. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYWIG 5
DB 38 TYWIG 42
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```
AC O8IGH9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RH13862p (Fragment).
GN Name=Uevia; ORFNames=CG10640;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
DR EMBL; BT001776; AAN71531.1; -; mRNA.
DR HSPF; P53152; 1JAT.
DR Ensemble; CG10640; Drosophila melanogaster.
DR FlyBase; FBgn0035601; CG10640.
DR FlyBase; FBgn0035601; Uevia.
DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR000608; UBO-conjugat_E2.
DR Pfam; PF00179; UQ con; 1.
DR ProDom; PD000463; UBO_conjugat; 1.
DR SMART; SM00212; UBCC; 1.
DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
FT NON TER 1
SQ SEQUENCE 137 AA; 15891 MW; 9AFC78A7F22EDC3 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. NO. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYWIG 5
DB 38 TYWIG 42

RESULT 3
O9VRL1 DROME
ID O9VRL1_DROME PRELIMINARY; PRT; 145 AA.

Query Match 100.0%; Score 33; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. NO. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYWIG 5
DB 38 TYWIG 42
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Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

[7]

RN NUCLEOTIDE SEQUENCE.
RRP STRAIN-Berkeley;
RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Paaleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnikier S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RLL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003566; AAF50784.1; -; Genomic_DNA.
DDR EMBL; AY060384; AAL25423.1; -; mRNA.
DR HSSP; F53152; 1JAT.
DR Ensembl; CG10640; Drosophila melanogaster.
DR FlyBase; FBgn0035601; CG10640.
DR FlyBase; FBgn0035601; UevIA.
DR GO; GO:0004840; P:ubiquitin conjugating enzyme activity; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR000608; UBQ-conjugat_E2.
DR Pfam; PF00179; UQ_con; 1.
DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
SQ SEQUENCE 145 AA; 16669 MW; BDF49A10486E0D8C CRC64;

Query Match 100.0%; Score 33; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gap

OY 1 TYWIG 5
|||||
Db 46 TYWIG 50

RESULT 4

Q6XI25 DROYA PRELIMINARY; PRT; 145 AA.
ID Q6XI25 DROYA PRELIMINARY;
AC Q6XI25;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to drosophila melanogaster Cg10640 (Fragment).
OS Drosophila yakuba (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7245;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887302; PubMed=14525923; DOI=10.1101/gr.1311003;
RR Domazet-Lozo T., Tautz D.;
RT "An evolutionary analysis of orphan genes in Drosophila.";
RL Genome Res. 13:2213-2219(2003).
CC -!- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
DR EMBL; AY232007; AARI0030.1; -; mRNA.
DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR000608; UBQ-conjugat_E2.
DR Pfam; PF00179; UQ_con; 1.
DR ProDom; PD000461; UBQ_conjugat; 1.
DR SMART; SMO0212; UBCC; 1.
DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
FT NON_TER 1
FT TER 145
SQ SEQUENCE 145 AA; 16669 MW; BDF49A10486E0D8C CRC64;

Query Match 100.0%; Score 33; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gap

```
RESULT 5
Q8WIA2_ORYSA PRELIMINARY; PRT; 150 AA.
ID Q8WIA2_ORYSA PRELIMINARY; PRT; 150 AA.
AC Q8WIA2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative villin-like protein (Fragment).
GN Name=VLN;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Niu X.G., Wang X.C., Liu Q.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF452250; AAL50774.1; -, mRNA.
DR Gramene; Q8WIA2; -.
DR GO; GO:0003779; F-actin binding; IEA.
DR InterPro; IPR007122; Gelsolin.
DR PRINTS; PR00597; GELSOLIN.
FT NON_TER 1 150
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16496 MW; 92B815FA4D3BF804 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 108 TYWIG 112

RESULT 6
Q9UDK8_HUMAN PRELIMINARY; PRT; 166 AA.
ID Q9UDK8_HUMAN PRELIMINARY; PRT; 166 AA.
AC Q9UDK8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 3 beta-hydroxysteroid dehydrogenase (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA McBride M.W., Russell A.J., Vass K., Forster V., Burridge S.M.,
RA Morrison N., Boyd E., Ponder B.A., Sutcliffe R.G.;
RT "New members of the 3 beta-hydroxysteroid dehydrogenase gene family.";
RL Mol. Cell. Probes 9:121-128(1995).
DR Ensembl; ENSG00000187197; Homo sapiens.
DR GO; GO:0030283; F:3(or 17)beta-hydroxysteroid dehydrogenase a. . .; TAS.
DR InterPro; IPR002225; 3beta_HSD.
DR Pfam; PF01073; 3beta_HSD; 2.
FT NON_TER 1 166
FT NON_TER 166 166
FT NON_CONS 53 54
FT NON_TER 166 166
SQ SEQUENCE 166 AA; 19346 MW; 0D2DB98CBA7C812D CRC64;

Query Match 100.0%; Score 33; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 84 TYWIG 88

RESULT 7
YPEV_LACDL STANDARD; PRT; 175 AA.
ID YPEV_LACDL STANDARD; PRT; 175 AA.
AC P45495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical transport protein in pepv 3'region (ORF2) (Fragment).
OS Lactobacillus delbrueckii subsp. lactis.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=29397;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=DSM 7290 / WS87;
RX MEDLINE=95093606; PubMed=7528082;
RA Vongerichten K., Klein J., Matern H., Plapp R.;
RT "Cloning and nucleotide sequence analysis of pepv, a carnosinase gene
from Lactobacillus delbrueckii subsp. lactis DSM 7290, and partial
characterization of the enzyme.";
RL Microbiology 140:2591-2600(1994).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -!- SIMILARITY: Belongs to the amino acid-polyamine-organocation (APC)
superfamily.
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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CC EMBL; Z31377; CAA83253.1; -, Genomic DNA.
CC PIR; S57903; S57903.
CC InterPro; IPR002293; AA/rel_permease1.
CC InterPro; IPR004840; AAC_permease.
CC InterPro; IPR004841; Permease_region.
CC PANTHER; PTHR11785; AA/rel_permease1; 1.
CC Pfam; PF00324; AA_permease; 1.
CC PROSITE; PS00218; AMINO ACID PERMEASE_1; 1.
KW Amino-acid transport; Hypothetical protein; Transmembrane; Transport.
FT TRANSMEM 25 45 Potential.
FT TRANSMEM 46 66 Potential.
FT TRANSMEM 97 117 Potential.
FT TRANSMEM 124 144 Potential.
FT TRANSMEM 155 175 Potential.
FT NON_TER 175 175
SQ SEQUENCE 175 AA; 19239 MW; A3BABF17736B9C63 CRC64;

Query Match 100.0%; Score 33; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 101 TYWIG 105

RESULT 8
Q4MRV1_BACCE PRELIMINARY; PRT; 178 AA.
ID Q4MRV1_BACCE PRELIMINARY; PRT; 178 AA.
AC Q4MRV1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORENAMES=BCE_G9241_4402;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasgo D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Malden M.C.J., Priest E.G., Barker M., Jiang L., Cer R.Z.,
RA Rillstone J., Peterson S.N., Meyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDJB whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAEX01000010; EAL14898.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 178 AA; 20245 MW; 7335039A2DE9847A CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 32 TYWIG 36

RESULT 9
Q6HDH2_BACHK
ID Q6HDH2_BACHK PRELIMINARY; PRT; 178 AA.
AC Q6HDH2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=B79727.4086;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=97-27;
RA Brittin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RA "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DDJB databases.
DR EMBL; AE017355; AAT62860.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 178 AA; 20384 MW; 0EA5F67C129A1802 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 32 TYWIG 36

RESULT 10
Q73014_BACCI
ID Q73014_BACCI PRELIMINARY; PRT; 178 AA.
AC Q73014;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BC24432;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
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RN NUCLEOTIDE SEQUENCE.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasgo D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXOI.1";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017278; AAS43333.1; -; Genomic_DNA.
DR TIGR; BC84432; -.
KW Complete proteome.
SQ SEQUENCE 178 AA; 20187 MW; A4F6FCB8B6E51192 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 32 TYWIG 36

RESULT 11
Q818B8_BACCR
ID Q818B8_BACCR PRELIMINARY; PRT; 178 AA.
AC Q818B8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BC4347;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haseikorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017012; AAP11260.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 178 AA; 20184 MW; 66CAC78EF69F1489 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 32 TYWIG 36

RESULT 12
Q81LN5_BACAN
ID Q81LN5_BACAN PRELIMINARY; PRT; 178 AA.
AC Q81LN5; Q6HT42; Q6KMD0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BA4579, BAS4248, GBAA4579;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus anthracis group.
OX NCBI_TaxID=1392;
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RP NUCLEOTIDE SEQUENCE.
RC STRAINAmes / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.B., Tetelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason B., Rikstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.B., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAINAmes / isolate 0581;
RA Rayel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics."
RL Submitted (MAY-2004) to the ENBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.,
RT "Complete genome sequence of Bacillus anthracis Sterne."
RL Submitted (JAN-2004) to the ENBL/GenBank/DBJ databases.
DR EMBL; AE017038; AAP28286.1; -; Genomic DNA.
DR EMBL; AE017334; AAT33699.1; -; Genomic DNA.
DR EMBL; AE017225; AAT56547.1; -; Genomic_DNA.
DR TIGR; BA579; -.
DR TIGR; GBAA4579; -.
RW Complete proteome; Hypothetical protein.
SQ SEQUENCE 178 AA; 20212 MW; 73CF86CE8583764C CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 32 TYWIG 36

RESULT 13
Q634J1_BACCCZ PRELIMINARY; PRT; 178 AA.
AC Q634J1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN ORFNames=BCE33L4097;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.;
RT "Complete genome sequence of Bacillus cereus ZK."
RL Submitted (JUL-2004) to the ENBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU16170.1; -; Genomic DNA.
RW Complete proteome; Hypothetical protein.
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SQ SEQUENCE 178 AA; 20371 MW; E31E967C0C6BFF2A CRC64;

Query Match 100.0%; Score 33; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 32 TYWIG 36

RESULT 14
Q9RY56_DEIRA PRELIMINARY; PRT; 181 AA.
AC Q9RY56;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein DR0094.
GN OrderedLocustNames=DR0094;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RI."
RL Science 286:1571-1577(1999).
DR EMBL; AE001872; AAF09690.1; -; Genomic_DNA.
DR TIGR; DR0094; -.
RW Complete proteome; Hypothetical protein.
SQ SEQUENCE 181 AA; 19371 MW; E29394CD96C746A4 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 114 TYWIG 118

RESULT 15
Q8C634_MOUSE PRELIMINARY; PRT; 189 AA.
AC Q8C634;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4922502D21 product:hypothetical C-type lectin domain
DE containing protein, full insert sequence (similar to C lectin-related
DE protein A).
GN Name=4922502D21Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
```

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito K.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kouchiwa H.,
RA Kuehl P., Lewis S., Matsumoto Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka O.K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltas L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravitsky T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Iehil Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalil D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX Director MGC Project;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RA EMBL; AK076635; BAC36425.1; -; mRNA.
RA EMBL; BC089479; AA089479.1; -; mRNA.
RA EMBL; ENSMUSG0000047720; Mus musculus.
RA MGI; MGI:2685920; 4922502D21Rik.
RA GO; GO:0005529; F:sugar binding; IEA.
RA InterPro; IPR001304; LECTIN_C.
RA Pfam; PF00059; LECTIN_C; 1.
RA SMART; SM00034; LECTIN_1.
RA PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
RA Hypothetical protein; LECTIN.
SQ SEQUENCE 189 AA; 22107 MW; 2EE5673DBAC2B39E CRC64;

Query Match 100.0%; Score 33; DB 2; Length 189;

Best Local Similarity 100.0%; Pred. No. 4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0;

1 TYWIG 5

|||||

Db 127 TWIG 131

Search completed: December 3, 2005, 14:32:23
Job time : 11.8163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:24:58 ; Search time 2.12245 Seconds
(without alignments)
194.765 Million cell updates/sec

Title: US-10-769-144-13

Perfect score: 33

Sequence: 1 TYWIG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/PCTRUS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	88	2	US-09-726-219A-172
2	33	100.0	88	2	US-09-196-522-172
3	33	100.0	151	2	US-09-270-767-44527
4	33	100.0	430	2	US-09-328-352-5453
5	32	97.0	383	2	US-09-902-540-11130
6	32	97.0	415	2	US-09-902-540-9936
7	32	97.0	616	2	US-09-540-236-3084
8	31	93.9	5	2	US-09-920-262A-1
9	31	93.9	110	2	US-09-252-991A-18248
10	31	93.9	119	2	US-09-920-262A-7
11	31	93.9	315	2	US-09-603-208A-212
12	31	93.9	483	2	US-09-603-208A-210
13	31	93.9	484	2	US-09-328-352-4849
14	31	93.9	488	2	US-09-328-352-4928
15	30	90.9	476	2	US-09-328-352-5950
16	29	87.9	8	2	US-08-444-818-602
17	29	87.9	8	2	US-08-444-818-603
18	29	87.9	8	2	US-08-444-818-604
19	29	87.9	98	1	US-08-478-039-81
20	29	87.9	98	1	US-08-476-349A-81
21	29	87.9	98	1	US-08-665-202-33
22	29	87.9	98	2	US-09-315-574-33
23	29	87.9	98	2	US-10-194-975-45
24	29	87.9	117	2	US-08-545-809A-133
25	29	87.9	117	2	US-09-515-697-133
26	29	87.9	119	2	US-09-025-769B-26
27	29	87.9	119	2	US-09-490-070A-26

28	29	87.9	119	2	US-09-490-153-26	Sequence 26, Appl
29	29	87.9	119	2	US-09-490-324-26	Sequence 26, Appl
30	29	87.9	120	2	US-09-025-769B-40	Sequence 40, Appl
31	29	87.9	120	2	US-09-025-769B-67	Sequence 67, Appl
32	29	87.9	120	2	US-09-490-070A-40	Sequence 40, Appl
33	29	87.9	120	2	US-09-490-070A-67	Sequence 67, Appl
34	29	87.9	120	2	US-09-490-153-40	Sequence 40, Appl
35	29	87.9	120	2	US-09-490-153-67	Sequence 67, Appl
36	29	87.9	120	2	US-09-490-324-40	Sequence 40, Appl
37	29	87.9	120	2	US-09-490-324-67	Sequence 67, Appl
38	29	87.9	121	1	US-08-388-672A-20	Sequence 20, Appl
39	29	87.9	121	1	US-08-388-672A-23	Sequence 23, Appl
40	29	87.9	121	2	US-09-080-554-23	Sequence 23, Appl
41	29	87.9	122	2	US-08-983-607-30	Sequence 30, Appl
42	29	87.9	126	2	US-09-080-554-20	Sequence 20, Appl
43	29	87.9	131	2	US-09-291-922-6	Sequence 6, Appl
44	29	87.9	165	2	US-09-902-540-9847	Sequence 9847, Ap
45	29	87.9	193	2	US-09-543-681A-4479	Sequence 4479, Ap

ALIGNMENTS

RESULT 1

US-09-726-219A-172
; Sequence 172, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-172

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Query Match      100.0%; Score 33; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 31 TYWIG 35

RESULT 2
US-09-196-522-172
; Sequence 172, Application US/09196522
; Patent No. 6916605
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-0004
; CURRENT APPLICATION NUMBER: US/09/196,522
; CURRENT FILING DATE: 1998-11-28
; PRIOR FILING DATE: 1998-11-28
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-196-522-172

Query Match      100.0%; Score 33; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 31 TYWIG 35

RESULT 3
US-09-270-767-44527
; Sequence 44527, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
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; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44527
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44527

Query Match      100.0%; Score 33; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 52 TYWIG 56

RESULT 4
US-09-328-352-5453
; Sequence 5453, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GPC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5453
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5453

Query Match      100.0%; Score 33; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 185 TYWIG 189

RESULT 5
US-09-902-540-11130
; Sequence 11130, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11130
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11130

Query Match      97.0%; Score 32; DB 2; Length 383;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5

Db 295 TYWVG 299

RESULT 6

US-09-902-540-9936
; Sequence 9936, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9936
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-9936

Query Match 97.0%; Score 32; DB 2; Length 415;

Best Local Similarity 80.0%; Pred. No. 3.7e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5

Db 58 TYWVG 62

RESULT 7

US-09-540-236-3084
; Sequence 3084, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3084
; LENGTH: 616
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3084

Query Match 97.0%; Score 32; DB 2; Length 616;

Best Local Similarity 80.0%; Pred. No. 5.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5

Db 593 TYWVG 597

RESULT 8

US-09-920-262A-1
; Sequence 1, Application US/09920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie

; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-1

Query Match 93.9%; Score 31; DB 2; Length 5;

Best Local Similarity 80.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5

Db 1 TYWLG 5

RESULT 9

US-09-252-991A-18248
; Sequence 18248, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18248
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18248

Query Match 93.9%; Score 31; DB 2; Length 110;

Best Local Similarity 80.0%; Pred. No. 1.6e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5

Db 85 TYWLG 89

RESULT 10

US-09-920-262A-7
; Sequence 7, Application US/09920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358

;
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-7

Query Match 93.9%; Score 31; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
|||:|
Db 31 TYWIG 35

RESULT 11
US-09-603-208A-212
; Sequence 212, Application US/09603208A
; Patent No. 6822084
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; APPLICANT: Lee, Heung-Shick
; APPLICANT: Kim, Hyung-Joon
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
; FILE REFERENCE: BGI-124CP
; CURRENT APPLICATION NUMBER: US/09/603,208A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142692
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/151214
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930429.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931413.6
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931457.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931541.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941382.7
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 306
; SEQ ID NO 212
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-603-208A-212

Query Match 93.9%; Score 31; DB 2; Length 315;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
|||:|

Db 129 TYWIG 133
|||:|

RESULT 12
US-09-603-208A-210
; Sequence 210, Application US/09603208A
; Patent No. 6822084
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; APPLICANT: Lee, Heung-Shick
; APPLICANT: Kim, Hyung-Joon
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
; FILE REFERENCE: BGI-124CP
; CURRENT APPLICATION NUMBER: US/09/603,208A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142692
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/151214
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930429.7
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931413.6
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931457.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931541.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941382.7
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 306
; SEQ ID NO 210
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-603-208A-210

Query Match 93.9%; Score 31; DB 2; Length 483;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
|||:|

Db 129 TYWIG 133
|||:|

RESULT 13
US-09-328-352-4849
; Sequence 4849, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252

Query Match 93.9%; Score 31; DB 2; Length 483;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
|||:|

Db 129 TYWIG 133
|||:|

RESULT 13
US-09-328-352-4849
; Sequence 4849, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252

Query Match 93.9%; Score 31; DB 2; Length 315;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
|||:|

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; SEQ ID NO 4849
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4849

Query Match      93.9%; Score 31; DB 2; Length 484;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
      |||:|
Db      111 TYWLG 115

RESULT 14
US-09-328-352-4928
; Sequence 4928, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4928
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4928

Query Match      93.9%; Score 31; DB 2; Length 488;
Best Local Similarity 80.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
      |||:|
Db      112 TYWLG 116

RESULT 15
US-09-328-352-5950
; Sequence 5950, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5950
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5950

Query Match      90.9%; Score 30; DB 2; Length 476;
Best Local Similarity 80.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
      |||:|
Db      257 TYWVG 261

Search completed: December 3, 2005, 14:11:29
Job time : 2.12245 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:27:13 ; Search time 6.85714 Seconds
(without alignments)
304.667 Million cell updates/sec

Title: US-10-769-144-13

Perfect score: 33

Sequence: 1 TYWIG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	5	4	US-10-374-932-5
2	33	100.0	5	4	US-10-379-741-5
3	33	100.0	5	5	US-10-769-144-13
4	33	100.0	5	5	US-10-891-658-92
5	33	100.0	5	5	US-10-982-725-5
6	33	100.0	5	5	US-10-903-191-13
7	33	100.0	76	4	US-10-437-963-106931
8	33	100.0	88	4	US-10-803-622-172
9	33	100.0	88	4	US-10-803-653-172
10	33	100.0	116	3	US-09-851-614-4
11	33	100.0	116	4	US-10-035-637-4
12	33	100.0	116	5	US-10-769-144-4
13	33	100.0	116	5	US-10-903-191-4
14	33	100.0	125	5	US-10-891-658-79
15	33	100.0	130	4	US-10-226-615-2
16	33	100.0	130	4	US-10-374-932-2
17	33	100.0	130	4	US-10-379-741-2
18	33	100.0	130	5	US-10-982-725-2
19	33	100.0	145	6	US-11-097-143-22335
20	33	100.0	248	3	US-09-880-748-1
21	33	100.0	248	4	US-10-293-418-1
22	33	100.0	373	4	US-10-114-270-92
23	33	100.0	393	4	US-10-425-115-208389
24	33	100.0	411	5	US-10-769-144-12
25	33	100.0	411	5	US-10-903-191-12
26	33	100.0	468	5	US-10-769-144-2
27	33	100.0	468	5	US-10-903-191-2

Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 126524,
Sequence 3838, Ap
Sequence 262693,
Sequence 880, App
Sequence 48326, A
Sequence 165309,
Sequence 22427, A
Sequence 142529,
Sequence 48506, A
Sequence 4, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-374-932-5

; Sequence 5, Application US/10374932

; Publication No. US20030235586A1

; GENERAL INFORMATION:

; APPLICANT: van de Winkel, Jan G.J.

; APPLICANT: van Dijk, Marcus Antonius

; APPLICANT: Schuurman, Janine

; APPLICANT: Gerritsen, Arnout F.

; APPLICANT: Baadsgaard, Ole

; APPLICANT: Petersen, Jorgen

; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)

; FILE REFERENCE: GMI-024CP

; CURRENT APPLICATION NUMBER: US/10/374,932

; CURRENT FILING DATE: 2003-02-26

; PRIOR APPLICATION NUMBER: US 60/314,731

; PRIOR FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: US 10/226615

; PRIOR FILING DATE: 2002-08-23

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-374-932-5

Query Match 100.0%; Score 33; DB 4; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5

Db 1 TYWIG 5

RESULT 2

US-10-379-741-5

; Sequence 5, Application US/10379741

; Publication No. US20040071702A1

; GENERAL INFORMATION:

; APPLICANT: van de Winkel, Jan G.J.

; APPLICANT: van Dijk, Marcus Antonius

; APPLICANT: Schuurman, Janine

; APPLICANT: Gerritsen, Arnout F.

; APPLICANT: Baadsgaard, Ole

; APPLICANT: Petersen, Jorgen

; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)

; FILE REFERENCE: GMI-024CP2

; CURRENT APPLICATION NUMBER: US/10/379,741

; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 10/226615
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-741-5

Query Match 100.0%; Score 33; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 1 TYWIG 5

RESULT 3
US-10-769-144-13
; Sequence 13, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-13

Query Match 100.0%; Score 33; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 1 TYWIG 5

RESULT 4
US-10-891-658-92
; Sequence 92, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15

; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 92
; LENGTH: 5
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-92

Query Match 100.0%; Score 33; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 1 TYWIG 5

RESULT 5
US-10-982-725-5
; Sequence 5, Application US/10982725
; Publication No. US20050123542A1
; GENERAL INFORMATION:
; APPLICANT: BEURSKENS, Frank
; APPLICANT: SCHURMAN, Janine
; APPLICANT: PARREN, Paul
; APPLICANT: PETERSEN, Jorgen
; APPLICANT: BAADSGAARD, Ole
; TITLE OF INVENTION: METHODS FOR TREATING DISORDERS INVOLVING MONOCYTES
; FILE REFERENCE: AMJ-002
; CURRENT APPLICATION NUMBER: US/10/982,725
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518552
; PRIOR FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-725-5

Query Match 100.0%; Score 33; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
Db 1 TYWIG 5

RESULT 6
US-10-903-191-13
; Sequence 13, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-903-191-13

Query Match      100.0%; Score 33; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
Db 1 TYWIG 5

RESULT 7
US-10-437-963-106931
; Sequence 106931, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106931
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_11330C.1.pap
US-10-437-963-106931

Query Match      100.0%; Score 33; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
Db 9 TYWIG 13

RESULT 8
US-10-803-622-172
; Sequence 172, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
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; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-803-622-172

Query Match      100.0%; Score 33; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWIG 5
Db 31 TYWIG 35

RESULT 9
US-10-803-653-172
; Sequence 172, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
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; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-803-653-172

Query Match      100.0%; Score 33; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
Db      31 TYWIG 35

RESULT 10
US-09-851-614-4
; Sequence 4, Application US/09851614
; Publication No. US20030167502A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MXI-166
; CURRENT APPLICATION NUMBER: US/09/851,614
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-614-4

Query Match      100.0%; Score 33; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
Db      31 TYWIG 35

RESULT 11
US-10-035-637-4
; Sequence 4, Application US/10035637
; Publication No. US20030031667A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035,637
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/851,614
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-035-637-4

Query Match      100.0%; Score 33; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
Db      31 TYWIG 35

RESULT 12
US-10-769-144-4
; Sequence 4, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-4

Query Match      100.0%; Score 33; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYWIG 5
Db      31 TYWIG 35

RESULT 13
US-10-903-191-4
; Sequence 4, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-4
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Query Match 100.0%; Score 33; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
|
|
|
|
Db 31 TYWIG 35

RESULT 14
US-10-891-658-79
; Sequence 79, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-79

Query Match 100.0%; Score 33; DB 5; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
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|
|
|
Db 31 TYWIG 35

RESULT 15
US-10-226-615-2
; Sequence 2, Application US/10226615
; Publication No. US20030138421A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus Antonius
; APPLICANT: Gerritsen, Arnout F.
; APPLICANT: Schuurman, Janine
; APPLICANT: Baadsgaard, Ole
; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
; FILE REFERENCE: GMI-024
; CURRENT APPLICATION NUMBER: US/10/226,615
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-226-615-2

Query Match 100.0%; Score 33; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
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|
|
|
Db 31 TYWIG 35

Search completed: December 3, 2005, 14:17:34
Job time : 6.85714 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:48:29 ; Search time 0.285714 Seconds
(without alignments)
83.796 Million cell updates/sec

Title: US-10-769-144-13

Perfect score: 33

Sequence: 1 TYWIG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	248	7	US-11-054-515-1
2	29	87.9	98	7	US-11-054-669-45
3	29	87.9	98	7	US-11-084-554-56
4	29	87.9	252	7	US-11-054-515-1537
5	28	84.8	157	6	US-10-793-626-1168
6	28	84.8	163	6	US-10-467-657-6140
7	28	84.8	249	7	US-11-054-515-1312
8	28	84.8	254	7	US-11-054-515-873
9	28	84.8	254	7	US-11-054-515-888
10	28	84.8	254	7	US-11-054-515-1087
11	28	84.8	254	7	US-11-054-515-1088
12	28	84.8	372	6	US-10-844-035-1
13	28	84.8	582	7	US-11-074-176-110
14	27	81.8	117	6	US-10-821-234-1253
15	27	81.8	314	7	US-11-108-172-1110
16	27	81.8	372	6	US-10-131-826A-106
17	27	81.8	416	6	US-10-821-234-1375
18	26	78.8	118	6	US-10-793-626-2630
19	26	78.8	130	6	US-10-467-657-3470
20	26	78.8	163	6	US-10-467-657-8522
21	26	78.8	178	6	US-10-467-657-2108
22	26	78.8	232	6	US-10-793-626-1602
23	26	78.8	244	6	US-10-821-234-1264
24	26	78.8	253	7	US-11-054-515-1003
25	26	78.8	253	7	US-11-054-515-1007

26	26	78.8	265	6	US-10-689-742-188	Sequence 188, Appl
27	26	78.8	293	6	US-10-131-826A-422	Sequence 422, Appl
28	26	78.8	361	6	US-10-821-234-1166	Sequence 1166, Appl
29	26	78.8	433	6	US-10-131-826A-6	Sequence 6, Appl
30	26	78.8	491	6	US-10-131-826A-278	Sequence 278, Appl
31	26	78.8	493	6	US-10-131-826A-268	Sequence 268, Appl
32	26	78.8	493	7	US-10-067-121-10	Sequence 10, Appl
33	26	78.8	493	7	US-11-067-121-20	Sequence 20, Appl
34	26	78.8	496	7	US-11-067-121-3	Sequence 3, Appl
35	26	78.8	496	7	US-11-067-121-12	Sequence 12, Appl
36	26	78.8	501	7	US-11-055-822-52	Sequence 52, Appl
37	26	78.8	515	6	US-10-467-657-1968	Sequence 1968, Appl
38	26	78.8	613	6	US-10-131-826A-190	Sequence 190, Appl
39	26	78.8	617	6	US-10-982-545-2	Sequence 2, Appl
40	26	78.8	782	6	US-10-821-234-1592	Sequence 1592, Appl
41	26	78.8	2323	6	US-10-793-626-760	Sequence 760, Appl
42	25	75.8	146	6	US-10-793-626-2694	Sequence 2694, Appl
43	25	75.8	148	6	US-10-512-109-21	Sequence 21, Appl
44	25	75.8	214	6	US-10-793-626-1898	Sequence 1898, Appl
45	25	75.8	224	6	US-10-793-626-1002	Sequence 1002, Appl

ALIGNMENTS

RESULT 1

US-11-054-515-1
; Sequence 1, Application US/11054515
; Publication No US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1

Query Match 100.0%; Score 33; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 6.1; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 TYWIG 5

Db 31 TYWIG 35

RESULT 2

US-11-054-669-45
; Sequence 45, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-45

Query Match 87.9%; Score 29; DB 7; Length 98;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
:||||
Db 31 SYWIG 35

RESULT 3
US-11-084-554-56
; Sequence 56, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-56

Query Match 87.9%; Score 29; DB 7; Length 98;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
:||||
Db 31 SYWIG 35

RESULT 4
US-11-054-515-1537
; Sequence 1537, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1537
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1537

Query Match 87.9%; Score 29; DB 7; Length 252;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWIG 5
:||||
Db 31 SYWIG 35

RESULT 5
US-10-793-626-1168
; Sequence 1168, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1168
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1168

Query Match 84.8%; Score 28; DB 6; Length 157;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5
:||||
Db 112 YWIG 115

RESULT 6
US-10-467-657-6140
; Sequence 6140, Application US/10467657

Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6140
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6140

Query Match 84.8%; Score 28; DB 6; Length 163;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5
Db 113 YWIG 116

RESULT 7

US-11-054-515-1312
; Sequence 1312, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1312
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1312

Query Match 84.8%; Score 28; DB 7; Length 249;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5

Db 32 YWIG 35

RESULT 8

US-11-054-515-873
; Sequence 873, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 873
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-873

Query Match 84.8%; Score 28; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWIG 5
Db 32 YWIG 35

RESULT 9

US-11-054-515-888
; Sequence 888, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15

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; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 888
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-888

Query Match      84.8%; Score 28; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YWIG 5
Db      32 YWIG 35

RESULT 10
US-11-054-515-1087
; Sequence 1087, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1087
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1088

Query Match      84.8%; Score 28; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YWIG 5
Db      32 YWIG 35

RESULT 11
US-11-054-515-1087
; Sequence 1087, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1087
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1088

Query Match      84.8%; Score 28; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YWIG 5
Db      32 YWIG 35

RESULT 12
US-10-844-035-1
; Sequence 1, Application US/10844035
; Publication No. US20050255098A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, STEVEN D.
; APPLICANT: NOBLE, LINDA J.
; TITLE OF INVENTION: METHODS OF TREATING TRAUMATIC SPINAL
; TITLE OF INVENTION: CORD INJURY
; FILE REFERENCE: UCAL-319
; CURRENT APPLICATION NUMBER: US/10/844,035
; CURRENT FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 372
; TYPE: PRT
; ORGANISM: homo sapien
US-10-844-035-1

Query Match      84.8%; Score 28; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YWIG 5
Db      87 YWIG 90
```

```
US-11-054-515-1088
; Sequence 1088, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1088
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1088

Query Match      84.8%; Score 28; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YWIG 5
Db      32 YWIG 35

RESULT 12
US-10-844-035-1
; Sequence 1, Application US/10844035
; Publication No. US20050255098A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, STEVEN D.
; APPLICANT: NOBLE, LINDA J.
; TITLE OF INVENTION: METHODS OF TREATING TRAUMATIC SPINAL
; TITLE OF INVENTION: CORD INJURY
; FILE REFERENCE: UCAL-319
; CURRENT APPLICATION NUMBER: US/10/844,035
; CURRENT FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 372
; TYPE: PRT
; ORGANISM: homo sapien
US-10-844-035-1

Query Match      84.8%; Score 28; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YWIG 5
Db      87 YWIG 90
```

RESULT 13

US-11-074-176-110
; Sequence 110, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaeshammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Perill, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-110

Query Match 84.8%; Score 28; DB 7; Length 582;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWIG 5
|||
DB 128 YWIG 131

RESULT 14

US-10-821-234-1253
; Sequence 1253, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1253
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1253

Query Match 81.8%; Score 27; DB 6; Length 117;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWIG 5
|||
DB 68 YWIG 71

RESULT 15

US-11-108-172-1110
; Sequence 1110, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stoik, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1110
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-1110

Query Match 81.8%; Score 27; DB 7; Length 314;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYWI 4
|||
DB 141 TYWI 144

Search completed: December 3, 2005, 14:17:54
Job time : 0.285714 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:10:00 ; Search time 29.0735 Seconds
(without alignments)
256.916 Million cell updates/sec

Title: US-10-769-144-14

Perfect score: 92

Sequence: 1 IIPGDSDTIYSPSQFQ 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	17	ADR46831	Adr46831 Human ant
2	92	100.0	116	Aam48005	Aam48005 Human mon
3	92	100.0	116	ADR46821	Adr46821 Human ant
4	92	100.0	411	ADR46829	Adr46829 Human p81
5	92	100.0	468	ADR46819	Adr46819 Human ant
6	92	100.0	613	ADR46827	Adr46827 Human bet
7	88	95.7	247	ADR28066	Adr28066 NPB polyp
8	85	92.4	17	ABR01560	ABR01560 Human ant
9	85	92.4	17	ABU08151	ABU08151 ErbB2 rec
10	85	92.4	17	ADD69218	ADD69218 Human hea
11	85	92.4	17	ADD69224	ADD69224 Human hea
12	85	92.4	17	ADD69221	ADD69221 Human hea
13	85	92.4	17	ADD69227	ADD69227 Human hea
14	85	92.4	17	ADD69230	ADD69230 Human hea
15	85	92.4	17	ADH89396	ADH89396 Human tra
16	85	92.4	17	ADP47140	ADP47140 Human pho
17	85	92.4	17	ADP47176	ADP47176 Human pho
18	85	92.4	17	ADP47158	ADP47158 Human pho
19	85	92.4	17	ADP47173	ADP47173 Human pho
20	85	92.4	17	ADS87942	ADS87942 Anti-IFN-
21	85	92.4	17	ADS94939	ADS94939 Anti-IFN-
22	85	92.4	17	ADR69906	ADR69906 Human IL-
23	85	92.4	17	ADX15527	ADX15527 Human ant
24	85	92.4	17	ADY26778	ADY26778 Human ant

25	85	92.4	17	9	AEA18876	Aea18876 Amino aci
26	85	92.4	84	2	AAW62797	Aaw62797 Amino aci
27	85	92.4	98	2	AAW54008	Aaw54008 Human ant
28	85	92.4	98	5	ABG78233	Abg78233 Human Fv
29	85	92.4	98	5	ABG78231	Abg78231 Human Fv
30	85	92.4	98	5	ABG78232	Abg78232 Human Fv
31	85	92.4	98	5	ABG91924	Abg91924 Human ant
32	85	92.4	98	5	ABG91922	Abg91922 Human ant
33	85	92.4	98	5	ABG91923	Abg91923 Human ant
34	85	92.4	98	6	ABU56809	Abu56809 Human Imm
35	85	92.4	98	6	ABP56508	Abp56508 Human ant
36	85	92.4	98	6	ABJ18687	Abj18687 Antibody
37	85	92.4	98	6	ABO27112	ABO27112 Human ger
38	85	92.4	98	7	ADD69247	ADD69247 Human hea
39	85	92.4	98	7	ADF10156	Adf10156 Antibody
40	85	92.4	98	7	ADF09948	Adf09948 Antibody
41	85	92.4	98	7	ADF10053	Adf10053 VEGF anti
42	85	92.4	98	7	ADK18943	Adk18943 Anti-huma
43	85	92.4	98	7	ADK18888	Adk18888 Anti-huma
44	85	92.4	98	7	ADK18877	Adk18877 Anti-huma
45	85	92.4	98	7	ADK18878	Adk18878 Anti-huma

ALIGNMENTS

RESULT 1

ADR46831

ID ADR46831 standard; peptide; 17 AA.

XX AC ADR46831;

XX DT 18-NOV-2004 (first entry)

XX DE Human antibody B11 heavy chain variable region CDR2 SEQ ID NO:14.

XX KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW betahCG; beta chorionic gonadotropin; antibody;
KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW antibody B11; heavy chain variable region; CDR;
KW complementarity determining region.

XX OS Homo sapiens.

XX PN WO2004074432-A2.

XX PD 02-SEP-2004.

XX PF 30-JAN-2004; 2004WO-US002725.

XX PR 31-JAN-2003; 2003US-0443979P.

XX PA (MEDA-) MEDAREX INC.

XX PI Keler T, Endres M, He L, Ramakrishna V;

XX WPI; 2004-635555/61.

XX PT New molecular conjugate having a monoclonal antibody that binds to human
APCs linked to a beta human chorionic gonadotropin, useful for inducing a
cytotoxic T cell response in cancers and infectious diseases.

XX PS Claim 8; SEQ ID NO 14; 82pp; English.

XX CC The present invention describes a molecular conjugate comprising a
monoclonal antibody that binds to human antigen presenting cells (APCs)
linked to beta human chorionic gonadotropin (betahCG), where the antibody
comprises a heavy and/or light chain variable region derived from a human
VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences

of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to betahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents the human antibody B11 heavy chain variable region complementarity determining region 2 (CDR2) amino acid sequence, which is used in the exemplification of the present invention.

Sequence 17 AA;

Query Match 100.0%; Score 92; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IYFGDSDTIYSPFQ 17
| | | | | | | | | | | | | | |
Db 1 IYFGDSDTIYSPFQ 17

RESULT 2
AAM48005
ID AAM48005 standard; protein; 116 AA.

XX AC AAM48005;

XX DT 08-MAR-2002 (first entry)

XX DE Human monoclonal antibody B11 variable heavy chain protein.

XX KW Human; monoclonal antibody; B11; antigen binding portion; dendritic cell; mannose receptor; growth; cytolysis; pathogen; virus; bacterium; autoimmune disease; inflammatory disorder; rheumatoid arthritis; multiple sclerosis; diabetes mellitus; immunomodulatory; antiinflammatory; antirheumatic; antidiabetic; neuroprotective; antidiabetic; antianaemic; endocrine; dermatological; antithyroid; uropathic; ophthalmological; muscular.

XX OS Homo sapiens.

XX PN WO200185798-A2.

XX PD 15-NOV-2001.

XX PF 08-MAY-2001; 2001WO-US015114.

XX PR 08-MAY-2000; 2000US-0203126P.

XX PR 07-SEP-2000; 2000US-0230739P.

XX PA (MEDA-) MEDAREX INC.
XX PI Deo YM, Keler T;
XX WPI; 2002-089788/12.
XX N-PSDB; ABA05500.

XX New human monoclonal antibodies specific for dendritic cells, useful for inhibiting growth or inducing cytolysis of a dendritic cell and treating or preventing a dendritic cell mediated disease, e.g., autoimmune disorders.

XX Example 2; Fig 13; 95pp; English.

XX The invention relates to human monoclonal antibodies or their antigen binding portions that specifically bind to dendritic cells and has one or more of the following characteristics: (a) a binding affinity constant to a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability to opsonise a dendritic cell; (c) the ability to internalise after binding to dendritic cells; or (d) the ability to activate dendritic cells. The isolated human monoclonal antibody or its antigen binding portion may also have any of the following characteristics: (a) mediates cytolysis of dendritic cells in the presence of human effector cells; or (b) inhibits growth of dendritic cells. The antibodies or its antigen binding portion, binds to and blocks the human mannose receptor on dendritic cells. The antibodies have immunomodulatory, antiinflammatory, antirheumatic, antarthritic, neuroprotective, antidiabetic, antianaemic, endocrine, dermatological, antithyroid, uropathic, ophthalmological and muscular activity. The antibodies or their antigen-binding fragments are useful for inhibiting growth of a dendritic cell, inducing cytolysis of a dendritic cell, treating or preventing a dendritic cell mediated disease, detecting the presence of a dendritic cell, targeting an antigen to a dendritic cell and preventing binding of a pathogen (a virus or a bacterium) to human mannose receptor on dendritic cells. In particular, the antibodies may be used to treat autoimmune disease, graft versus host disease, immune system or inflammatory disorders (e.g. rheumatoid arthritis), multiple sclerosis, diabetes mellitus, myasthenia gravis, pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's syndrome and Graves disease. The present sequence is that of the human monoclonal antibody B11 variable heavy chain, useful to the invention

Sequence 116 AA;

Query Match 100.0%; Score 92; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IYFGDSDTIYSPFQ 17
| | | | | | | | | | | | | | |
Db 50 IYFGDSDTIYSPFQ 66

RESULT 3

ADR46821

ID ADR46821 standard; protein; 116 AA.

XX AC ADR46821;

XX DT 18-NOV-2004 (first entry)

XX DE Human antibody B11 heavy chain variable region protein SEQ ID NO:4.

XX KW molecular conjugate; monoclonal antibody; human antigen presenting cell; antigen presenting cell; APC; human; beta human chorionic gonadotropin; betahCG; beta chorionic gonadotropin; antibody; T cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; antibody B11; heavy chain variable region.

XX OS Homo sapiens.

```

XX WO2004074432-A2.
XX
XX PD 02-SEP-2004.
XX
XX PF 30-JAN-2004; 2004WO-US002725.
XX
XX PR 31-JAN-2003; 2003US-0443979P.
XX
XX PA (MEDA-) MEDAREX INC.
XX
XX PI Keler T, Endres M, He L, Ramakrishna V;
XX
XX WPI; 2004-635555/61.
XX
XX DR N-PSDB; ADR46820.
XX
XX PT New molecular conjugate having a monoclonal antibody that binds to human
XX APCs linked to a beta human chorionic gonadotropin, useful for inducing a
XX cytotoxic T-cell response in cancers and infectious diseases.
XX
XX PS Claim 11; SEQ ID NO 4; 82pp; English.
XX
XX CC The present invention describes a molecular conjugate comprising a
XX monoclonal antibody that binds to human antigen presenting cells (APCs)
XX linked to beta human chorionic gonadotropin (betahCG), where the antibody
XX comprises a heavy and/or light chain variable region derived from a human
XX VH5-51 or Vκ-L15 germline sequence with the 98 or 95 amino acid sequences
XX of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
XX described: (1) a molecular conjugate comprising a human antibody heavy
XX chain and a human antibody light chain, where either or both chains are
XX linked to betahCG; (2) a molecular conjugate comprising a human single
XX chain antibody that binds to human APCs linked to betahCG, where the
XX conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
XX (ADR46829); (3) a composition comprising any of the molecular conjugates
XX as described above, and a carrier, optionally in combination with an
XX adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
XX against betahCG, comprising contacting any of the molecular conjugates
XX described above with APCs such that the antigen is processed and
XX presented to T cells in a manner which induces or enhances a T cell-
XX mediated response against the antigen; (5) immunising a subject
XX comprising administering any of the molecular conjugates described above,
XX optionally in combination with an adjuvant, a cytokine which stimulates
XX proliferation of dendritic cells and/or an immunostimulatory agent; and
XX (6) inducing or enhancing a cytotoxic T cell response against an antigen,
XX comprising forming a conjugate of the antigen and a monoclonal antibody
XX which binds to APCs, and contacting the conjugate either in vivo or ex
XX vivo with APCs such that the antigen is internalised, processed and
XX presented to T cells in a manner which induces or enhances a cytotoxic T
XX cell response against the antigen. The molecular conjugate has
XX cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
XX virucide and antimalarial activities, and can be used as a CD8 agonist,
XX for treating autoimmune disorders, cancers and infectious diseases by
XX eliciting a potent antigen-specific cytotoxic T lymphocyte response,
XX including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
XX herpes. The present sequence represents a human antibody B11 heavy chain
XX variable region, which is used in the exemplification of the present
XX invention.
XX
XX SQ Sequence 116 AA;
XX
XX Query Match 100.0%; Score 92; DB 8; Length 116;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 IYPGDSPTIYSPFQG 17
XX |||||||||||||||
XX Db 50 IYPGDSPTIYSPFQG 66
XX
XX RESULT 4
XX ADR46829

```

```

ID
XX
XX AC ADR46829;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Human pB11-betahCG molecular conjugate protein SEQ ID NO:12.
XX
XX KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
XX antigen presenting cell; APC; human; beta human chorionic gonadotropin;
XX betahCG; beta chorionic gonadotropin; antibody;
XX T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
XX immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
XX CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
XX melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
XX antibody B11; pB11-betahCG molecular conjugate; fusion protein.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX PN WO2004074432-A2.
XX
XX PD 02-SEP-2004.
XX
XX PF 30-JAN-2004; 2004WO-US002725.
XX
XX PR 31-JAN-2003; 2003US-0443979P.
XX
XX PA (MEDA-) MEDAREX INC.
XX
XX PI Keler T, Endres M, He L, Ramakrishna V;
XX
XX WPI; 2004-635555/61.
XX
XX DR N-PSDB; ADR46828.
XX
XX PT New molecular conjugate having a monoclonal antibody that binds to human
XX APCs linked to a beta human chorionic gonadotropin, useful for inducing a
XX cytotoxic T cell response in cancers and infectious diseases.
XX
XX PS Claim 16; SEQ ID NO 12; 82pp; English.
XX
XX CC The present invention describes a molecular conjugate comprising a
XX monoclonal antibody that binds to human antigen presenting cells (APCs)
XX linked to beta human chorionic gonadotropin (betahCG), where the antibody
XX comprises a heavy and/or light chain variable region derived from a human
XX VH5-51 or Vκ-L15 germline sequence with the 98 or 95 amino acid sequences
XX of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
XX described: (1) a molecular conjugate comprising a human antibody heavy
XX chain and a human antibody light chain, where either or both chains are
XX linked to betahCG; (2) a molecular conjugate comprising a human single
XX chain antibody that binds to human APCs linked to betahCG, where the
XX conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
XX (ADR46829); (3) a composition comprising any of the molecular conjugates
XX as described above, and a carrier, optionally in combination with an
XX adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
XX against betahCG, comprising contacting any of the molecular conjugates
XX described above with APCs such that the antigen is processed and
XX presented to T cells in a manner which induces or enhances a T cell-
XX mediated response against the antigen; (5) immunising a subject
XX comprising administering any of the molecular conjugates described above,
XX optionally in combination with an adjuvant, a cytokine which stimulates
XX proliferation of dendritic cells and/or an immunostimulatory agent; and
XX (6) inducing or enhancing a cytotoxic T cell response against an antigen,
XX comprising forming a conjugate of the antigen and a monoclonal antibody
XX which binds to APCs, and contacting the conjugate either in vivo or ex
XX vivo with APCs such that the antigen is internalised, processed and
XX presented to T cells in a manner which induces or enhances a cytotoxic T
XX cell response against the antigen. The molecular conjugate has
XX cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
XX virucide and antimalarial activities, and can be used as a CD8 agonist,
XX for treating autoimmune disorders, cancers and infectious diseases by
XX eliciting a potent antigen-specific cytotoxic T lymphocyte response,
XX including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
XX herpes. The present sequence represents a human antibody B11 heavy chain
XX variable region, which is used in the exemplification of the present
XX invention.
XX
XX SQ Sequence 116 AA;
XX
XX Query Match 100.0%; Score 92; DB 8; Length 116;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 IYPGDSPTIYSPFQG 17
XX |||||||||||||||
XX Db 50 IYPGDSPTIYSPFQG 66
XX
XX RESULT 4
XX ADR46829

```

CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC herpes. The present sequence represents a human pB1-betahCG molecular
CC conjugate, which is used in the exemplification of the present invention.
XX
SQ Sequence 411 AA;

Query Match 100.0%; Score 92; DB 8; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.5e-05; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;
Qy 1 IYIPGDSDTIYSPSFQ 17
Db 191 IYIPGDSDTIYSPSFQ 207
|||||

RESULT 5
ADR46819
ID ADR46819 standard; protein; 468 AA.

AC ADR46819;

DT 18-NOV-2004 (first entry)

DE Human antibody B11 heavy chain variable region protein SEQ ID NO:2.

XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
XX antigen presenting cell; APC; human; beta human chorionic gonadotropin;
XX betahCG; beta chorionic gonadotropin; antibody;
XX T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
XX immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
XX CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
XX melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
XX antibody B11; heavy chain variable region.

XX Homo sapiens.

XX WO2004074432-A2.

XX 02-SEP-2004.

XX 30-JAN-2004; 2004WO-US002725.

XX 31-JAN-2003; 2003US-0443979P.

XX (MEDA-) MEDAREX INC.

XX Keler T, Endres M, He L, Ramakrishna V;

XX WPI; 2004-635555/61.

XX N-PSDB; ADR46818.

XX New molecular conjugate having a monoclonal antibody that binds to human
PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
PT cytotoxic T cell response in cancers and infectious diseases.

XX Claim 13; SEQ ID NO 2; 82pp; English.

XX The present invention describes a molecular conjugate comprising a
CC monoclonal antibody that binds to human antigen presenting cells (APCs)
CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC comprises a heavy and/or light chain variable region derived from a human
CC VH5-51 or Vh-L15 germline sequence with the 98 or 95 amino acid sequences
CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
CC described: (1) a molecular conjugate comprising a human antibody heavy
CC chain and a human antibody light chain, where either or both chains are
CC linked to betahCG; (2) a molecular conjugate comprising a human single
CC chain antibody that binds to human APCs linked to betahCG, where the
CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC (ADR46829); (3) a composition comprising any of the molecular conjugates
CC as described above, and a carrier, optionally in combination with an
CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC against betahCG, comprising contacting any of the molecular conjugates

CC described above with APCs such that the antigen is processed and
CC presented to T cells in a manner which induces or enhances a T cell-
CC mediated response against the antigen; (5) immunising a subject
CC comprising administering any of the molecular conjugates described above,
CC optionally in combination with an adjuvant, a cytokine which stimulates
CC proliferation of dendritic cells and/or an immunostimulatory agent; and
CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC comprising forming a conjugate of the antigen and a monoclonal antibody
CC which binds to APCs, and contacting the conjugate either in vivo or ex
CC vivo with APCs such that the antigen is internalised, processed and
CC presented to T cells in a manner which induces or enhances a cytotoxic T
CC cell response against the antigen. The molecular conjugate has
CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC virucide and antimalarial activities, and can be used as a CD8 agonist,
CC and in vaccines. The methods and compositions of the present invention
CC are useful for inducing a cytotoxic T cell response, and in particular
CC for treating autoimmune disorders, cancers and infectious diseases by
CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC herpes. The present sequence represents a human antibody B11 heavy chain
CC variable region, which is used in the exemplification of the present
CC invention.

XX Sequence 468 AA;

Query Match 100.0%; Score 92; DB 8; Length 468;

Best Local Similarity 100.0%; Pred. No. 1.8e-05; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

Qy 1 IYIPGDSDTIYSPSFQ 17

Db 69 IYIPGDSDTIYSPSFQ 85
|||||

RESULT 6

ADR46827
ID ADR46827 standard; protein; 613 AA.

XX ADR46827;

XX 18-NOV-2004 (first entry)

XX Human betahCG-B11 molecular conjugate protein SEQ ID NO:10.

XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
XX antigen presenting cell; APC; human; beta human chorionic gonadotropin;
XX betahCG; beta chorionic gonadotropin; antibody;
XX T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
XX immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
XX CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
XX melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
XX antibody B11; betahCG-B11 molecular conjugate; fusion protein.

XX Homo sapiens.

XX Synthetic.

XX WO2004074432-A2.

XX 02-SEP-2004.

XX 30-JAN-2004; 2004WO-US002725.

XX 31-JAN-2003; 2003US-0443979P.

XX (MEDA-) MEDAREX INC.

XX Keler T, Endres M, He L, Ramakrishna V;

XX WPI; 2004-635555/61.

XX N-PSDB; ADR46826.

XX New molecular conjugate having a monoclonal antibody that binds to human
PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a

PT cytotoxic T cell response in cancers and infectious diseases.

XX Example 1; SEQ ID NO 10; 82pp; English.

XX The present invention describes a molecular conjugate comprising a
 CC monoclonal antibody that binds to human antigen presenting cells (APCs)
 CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
 CC comprises a heavy and/or light chain variable region derived from a human
 CC VH5-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences
 CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
 CC described: (1) a molecular conjugate comprising a human antibody heavy
 CC chain and a human antibody light chain, where either or both chains are
 CC linked to betahCG; (2) a molecular conjugate comprising a human single
 CC chain antibody that binds to human APCs linked to betahCG, where the
 CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
 CC (ADR46829); (3) a composition comprising any of the molecular conjugates
 CC as described above, and a carrier, optionally in combination with an
 CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
 CC against betahCG, comprising contacting any of the molecular conjugates
 CC described above with APCs such that the antigen is processed and
 CC presented to T cells in a manner which induces or enhances a T cell-
 CC mediated response against the antigen; (5) immunising a subject
 CC comprising administering any of the molecular conjugates described above,
 CC optionally in combination with an adjuvant, a cytokine which stimulates
 CC proliferation of dendritic cells and/or an immunostimulatory agent; and
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
 CC comprising forming a conjugate of the antigen and a monoclonal antibody
 CC which binds to APCs, and contacting the conjugate either in vivo or ex
 CC vivo with APCs such that the antigen is internalised, processed and
 CC presented to T cells in a manner which induces or enhances a cytotoxic T
 CC cell response against the antigen. The molecular conjugate has
 CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
 CC virucide and antimalarial activities, and can be used as a CD8 agonist,
 CC and in vaccines. The methods and compositions of the present invention
 CC are useful for inducing a cytotoxic T cell response, and in particular
 CC for treating autoimmune disorders, cancers and infectious diseases by
 CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
 CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
 CC herpes. The present sequence represents a human betahCG-B11 molecular
 CC conjugate, which is used in the exemplification of the present invention.

XX Sequence 613 AA;

Query Match 100.0%; Score 92; DB 8; Length 613;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0;

QY 1 IIPGSDTIYSPSQG 17
 |||||
 Db 69 IIPGSDTIYSPSQG 85

RESULT 7
 ADR28066
 ID ADR28066 standard; protein; 247 AA.

XX ADR28066;

XX 07-OCT-2004 (first entry)

XX NPB polypeptide scFv11, seq id 13.

XX Cytostatic; metastasis inhibitor; neuropilin binder; NPB; scFv;
 KW single chain antibody; neuropilin-1; NP-1; angiogenesis; tumour; cancer.

XX Mus sp.

XX Synthetic.

XX Key Location/Qualifiers

XX 89..105

XX /note= "complementary determining region claimed under
 claim 5"

PN WO2004056874-A2.

XX 08-JUL-2004.

XX 22-DEC-2003; 2003WO-EP014756.

XX 20-DEC-2002; 2002US-0435893P.

PR 15-JAN-2003; 2003EP-00000615.

XX (XERI-) XERION PHARM AG.

PA (TUFT) UNIV TUFTS.

XX Unger CM, Beste G, Zehetmeier C, Lain B, Torella C, Niewoehner J;
 PI Jay DG, Eustace BK, Knauer R, Jensen KH;

XX WPI; 2004-507700/48.

DR N-PSDB; ADR28100.

XX Novel neuropilin binder which is scFv, antibody fragment or bioconjugate,
 PT that modulates neuropilin-1 function or inhibits NP-1 dependent
 PT angiogenesis of endothelial cells and/or invasion of tumor cells useful
 PT for treating cancer.

XX Claim 3; SEQ ID NO 13; 120pp; English.

XX The invention relates to a neuropilin binder (NPB) (I) which is a
 CC polypeptide, antibody, scFv, antibody fragment or bioconjugate, that
 CC modulates neuropilin-1 (NP-1) function or inhibits NP-1 dependent
 CC angiogenesis of endothelial cells and/or invasion of tumour cells,
 CC whereby the NPB binds to NP-1 and modulates NP-1 function. Further
 CC disclosed is an ex vivo method of determining the dependency of the
 CC invasiveness of a naturally occurring invasive cancer cell on the
 CC functionality of NP-1. The NPB of the invention is an inhibitor of
 CC metastasis of NP-1 mediated invasion and/or adhesion and an inhibitor of
 CC tumour-associated NP-1 dependent angiogenesis. The NPB of the invention
 CC is useful for detecting NP-1 expression, modulation of NP-1 function,
 CC particularly modulation or inhibition of NP-dependent invasion or
 CC adhesion of cells, preferably tumour cells. It is useful in the
 CC manufacture of medicament for the treatment or prevention of NP-dependent
 CC angiogenesis and non-physiological blood vessel growth, particularly
 CC correlated with a tumour. It is also useful for treatment or prevention
 CC of cancer and/or metastasis of tumour cells. The current sequence
 CC represents a single chain antibody neuropilin binder (NPB) polypeptide.

XX Sequence 247 AA;

Query Match 95.7%; Score 88; DB 8; Length 247;
 Best Local Similarity 94.1%; Pred. No. 3.8e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIPGSDTIYSPSQG 17
 |||||
 Db 40 IIPGSDTIYSPSQG 56

RESULT 8

ABR01560

ID ABR01560 standard; peptide; 17 AA.

XX ABR01560;

XX 16-APR-2003 (first entry)

XX Human anti-TIMP-1 Fab VLCDR3 #48.

XX Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;
 KW matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;
 KW variable light chain; cytotactic; nephrotropic; cardiant; liver fibrosis;
 KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
 XX Homo sapiens.

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XX PN WO200286085-A2.
XX PD 31-OCT-2002.
XX PF 24-APR-2002; 2002WO-US012801.
XX PR 24-APR-2001; 2001US-0285683P.
XX PA (FARB ) BAYER CORP.
XX PA (MORP-) MORPHOSYS AG.
XX PI Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;
XX WPI, 2003-129114/12.
XX
XX PT New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies,
XX PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
XX PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung
XX PT cancer.
XX PS Claim 17; Page 226; 228pp; English.
XX
XX CC The invention relates to a novel purified preparation of a human
XX CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1)
XX CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP
XX CC -1. The antibody comprises a variable heavy chain (VHC)DR3 region and a
XX CC variable light chain (VLC)DR3 region. An antibody preparation of the
XX CC invention has hepatotropic, cytostatic, nephrotropic and cardiant
XX CC activity. The human antibody is useful for decreasing an MMP-inhibiting
XX CC activity of a TIMP-1. It is especially useful for ameliorating the
XX CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,
XX CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus
XX CC nephritis, glomerulosclerotic renal disease, idiopathic pulmonary
XX CC fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The
XX CC antibody is also useful for detecting a TIMP-1 in a test preparation, or
XX CC in diagnosing a disorder in which a TIMP-1 level is elevated. The
XX CC sequences shown in ABR01407-ABR01449 and ABR01555-ABR01569 represent
XX CC VLCDR regions of an antibody of the invention
XX
XX SQ Sequence 17 AA;
Query Match 92.4%; Score 85; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
| | | | | | | | | | | | | | |
Db 1 IYPGDSDTIYSPSFQ 17
| | | | | | | | | | | | | | |

RESULT 9
ABU08151
ID ABU08151 standard; peptide; 17 AA.
XX
XX AC ABU08151;
XX
XX DT 10-MAY-2003 (first entry)
XX
XX DE ErbB2 receptor antibody VH domain CDR-2.
XX
XX KW Human; single-chain antibody; anti-ErbB2 antibody; ErbB2; ErbB2
XX KW growth inhibitor; ErbB2 receptor; transmembrane tyrosine kinase receptor;
XX KW RTK; antibody; Gene therapy; bacteriophage; antitumor agent; tumour;
XX KW mammary carcinoma; ovarian carcinoma; colon carcinoma; lung carcinoma;
XX KW salivary gland tumour; gastric tumour; antiproliferative; cytostatic; VH;
XX KW CDR; complementarity determining region; variable domain; heavy chain.
XX
XX OS Homo sapiens.
XX
XX PN WO2003006509-A2.
XX
XX PD 23-JAN-2003.

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XX PF 10-JUL-2002; 2002WO-EP007671.
XX PR 10-JUL-2001; 2001IT-RM000408.
XX PA (UYNA-) UNIV NAPOLI STUDI FEDERICO II.
XX PI D'alessio G, Piccoli R, De Lorenzo C, Palmer DB, Ritter MA;
XX WPI, 2003-221720/21.
XX DR N-PSDB; ABX12974.
XX
XX PT New recombinant single-chain anti-ErbB2 antibody of human origin, useful
XX PT for pharmaceutical and diagnostic use, and as an antitumor agent for
XX PT mammary, ovarian, colon, lung carcinomas, salivary gland or gastric
XX PT tumore.
XX PS Claim 10; Page 8; 47pp; English.
XX
XX CC The invention discloses a recombinant single-chain anti-ErbB2 antibody of
XX CC human origin able to inhibit growth of cells expressing the ErbB2
XX CC receptor, referred to as ErbB2. The ErbB2 transmembrane tyrosine kinase
XX CC receptor (RTK) is highly expressed in breast, ovary and lung carcinomas
XX CC as well as salivary gland or gastric tumours. The antibodies, new
XX CC proteins, nucleotide sequences (gene therapy) and bacteriophage are
XX CC useful for pharmaceutical and diagnostic use, and as an antitumour agent,
XX CC where the tumour can be mammary, ovarian, colon, lung carcinomas,
XX CC salivary gland or gastric tumours. They are also useful in preparing
XX CC antiproliferative and antitumour drugs. The sequences presented are the
XX CC nucleic acids and encoded polypeptides that were used in the invention to
XX CC create the antibody
XX
XX SQ Sequence 17 AA;
Query Match 92.4%; Score 85; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
| | | | | | | | | | | | | | |
Db 1 IYPGDSDTIYSPSFQ 17
| | | | | | | | | | | | | | |

RESULT 10
ADD69218
ID ADD69218 standard; peptide; 17 AA.
XX
XX AC ADD69218;
XX
XX DT 15-JAN-2004 (first entry)
XX
XX DE Human heavy chain variable region CDR2 peptide - SEQ ID 22.
XX
XX KW monoclonal antibody; heavy chain variable region; light; framework;
XX KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
XX KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
XX KW colon cancer; renal carcinoma; gene therapy; human.
XX
XX OS Homo sapiens.
XX
XX PN WO20030064606-A2.
XX
XX PD 07-AUG-2003.
XX
XX PF 28-JAN-2003; 2003WO-US002448.
XX PR 28-JAN-2002; 2002US-00059989.
XX
XX PA (MEDA-) MEDAREX INC.
XX
XX PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX WPI, 2003-618360/58.

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XX New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
XX Claim 2; SEQ ID NO 22; 136pp; English.
XX
XX The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as doing gene therapy procedures. The current sequence is that of
CC the human heavy chain variable region CDR2 peptide of the invention.
XX
XX Sequence 17 AA;
SQ
Query Match 92.4%; Score 85; DB 7; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 I I Y P G D S D T Y S P S F Q G 17
Db 1 I I Y P G D S D T Y S P S F Q G 17
RESULT 11
ADD69224
ID ADD69224 standard; peptide; 17 AA.
XX
AC ADD69224;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human heavy chain variable region CDR2 peptide - SEQ ID 28.
XX
XX monoclonal antibody; heavy chain variable region; light; framework;
KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW colon cancer; renal carcinoma; gene therapy; human.
XX
XX Homo sapiens.
OS
XX WO2003064606-A2.
FN
XX 07-AUG-2003.
PD
XX 28-JAN-2003; 2003WO-US002448.
PF
XX 28-JAN-2002; 2002US-00059989.
XX
XX (MEDA-) MEDAREX INC.
PA
XX
XX Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
PI
XX WPI; 2003-618360/58.
FN
XX
XX New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
XX Claim 2; SEQ ID NO 28; 136pp; English.
PS
XX
XX The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4

CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as doing gene therapy procedures. The current sequence is that of
CC the human heavy chain variable region CDR2 peptide of the invention.
XX
XX Sequence 17 AA;
SQ
Query Match 92.4%; Score 85; DB 7; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 I I Y P G D S D T Y S P S F Q G 17
Db 1 I I Y P G D S D T Y S P S F Q G 17
RESULT 12
ADD69221
ID ADD69221 standard; peptide; 17 AA.
XX
AC ADD69221;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human heavy chain variable region CDR2 peptide - SEQ ID 25.
XX
XX monoclonal antibody; heavy chain variable region; light; framework;
KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW colon cancer; renal carcinoma; gene therapy; human.
XX
XX Homo sapiens.
OS
XX WO2003064606-A2.
FN
XX 07-AUG-2003.
PD
XX 28-JAN-2003; 2003WO-US002448.
PF
XX 28-JAN-2002; 2002US-00059989.
XX
XX (MEDA-) MEDAREX INC.
PA
XX
XX Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
PI
XX WPI; 2003-618360/58.
FN
XX
XX New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
XX Claim 2; SEQ ID NO 25; 136pp; English.
PS
XX
XX The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as doing gene therapy procedures. The current sequence is that of
CC the human heavy chain variable region CDR2 peptide of the invention.
XX
XX Sequence 17 AA;
SQ
Query Match 92.4%; Score 85; DB 7; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.1e-06;

```
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IIYPGDSDTYSPSFQ 17
Db 1 IIYPGDSDTYSPSFQ 17
RESULT 13
ID ADD69227 standard; peptide; 17 AA.
XX
AC ADD69227;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human heavy chain variable region CDR2 peptide - SEQ ID 31.
XX
KW monoclonal antibody; heavy chain variable region; light; framework;
KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW colon cancer; renal carcinoma; gene therapy; human.
XX
OS Homo sapiens.
XX
FN WO2003064606-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-US002448.
XX
PR 28-JAN-2002; 2002US-00059989.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX
FN WO2003064606-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-US002448.
XX
PR 28-JAN-2002; 2002US-00059989.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX
DR WPI; 2003-618360/58.
XX
PT New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
PS Claim 2; SEQ ID NO 31; 136pp; English.
XX
CC The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention or
CC demonstrates cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as during gene therapy procedures. The current sequence is that of
CC the human heavy chain variable region CDR2 peptide of the invention.
XX
SQ Sequence 17 AA;
Qy Query Match 92.4%; Score 85; DB 7; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IIYPGDSDTYSPSFQ 17
Db 1 IIYPGDSDTYSPSFQ 17
RESULT 14
ID ADD69230 standard; peptide; 17 AA.
XX
AC ADD69230;
XX
DT 15-APR-2004 (first entry)
XX
DE Human transferrin fusion protein-related CDR2 peptide SeqID40.
XX
KW fusion protein; transferrin protein; glycosylation;
KW antibody variable region; cytostatic; antibacterial; virucide;
KW antiparasitic; immunosuppressive; antiarthritic; gene therapy;
KW septic shock; endotoxin shock; cachexia syndrome; bacterial infection;
KW viral infection; parasitic infection; neoplasm; autoimmune disease;
KW arthritis; graft rejection.
XX
```

```
XX
DT 15-JAN-2004 (first entry)
XX
DE Human heavy chain variable region CDR2 peptide - SEQ ID 34.
XX
KW monoclonal antibody; heavy chain variable region; light; framework;
KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW colon cancer; renal carcinoma; gene therapy; human.
XX
OS Homo sapiens.
XX
FN WO2003064606-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-US002448.
XX
PR 28-JAN-2002; 2002US-00059989.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX
FN WO2003064606-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-US002448.
XX
PR 28-JAN-2002; 2002US-00059989.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX
DR WPI; 2003-618360/58.
XX
PT New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
PS Claim 2; SEQ ID NO 34; 136pp; English.
XX
CC The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention or
CC demonstrates cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as during gene therapy procedures. The current sequence is that of
CC the human heavy chain variable region CDR2 peptide of the invention.
XX
SQ Sequence 17 AA;
Qy Query Match 92.4%; Score 85; DB 7; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IIYPGDSDTYSPSFQ 17
Db 1 IIYPGDSDTYSPSFQ 17
RESULT 15
ID ADD69236 standard; peptide; 17 AA.
XX
AC ADD69236;
XX
DT 15-APR-2004 (first entry)
XX
DE Human transferrin fusion protein-related CDR2 peptide SeqID40.
XX
KW fusion protein; transferrin protein; glycosylation;
KW antibody variable region; cytostatic; antibacterial; virucide;
KW antiparasitic; immunosuppressive; antiarthritic; gene therapy;
KW septic shock; endotoxin shock; cachexia syndrome; bacterial infection;
KW viral infection; parasitic infection; neoplasm; autoimmune disease;
KW arthritis; graft rejection.
XX
```


OS Unidentified.
XX
XX US2003226155-A1.
XX
XX 04-DEC-2003.
XX
XX 10-MAR-2003; 2003US-00384060.
XX
XX 30-AUG-2001; 2001US-0315745P.
XX PR 30-NOV-2001; 2001US-0334059P.
XX PR 30-AUG-2002; 2002US-00231149A.
XX PR 30-AUG-2002; 2002US-0406977P.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
XX
XX Sadeghi H, Prior CP, Turner A;
XX
XX WPI; 2004-022093/02.
XX
XX New fusion protein comprising a transferrin protein exhibiting reduced
PT glycosylation fused to at least one antibody variable region, useful for
PT preparing a composition for treating e.g., septic shock, neoplasm or
PT autoimmune disease.
XX
XX Example 2; SEQ ID NO 40; 82pp; English.
XX
XX This invention relates to a novel fusion protein which comprises a
CC transferrin protein exhibiting reduced glycosylation fused to at least
CC one antibody variable region. The invention may be useful for the
CC development of compounds with cytostatic, antibacterial, virucide,
CC antiparasitic, immunosuppressive or antiarthritic activity. In addition,
CC the sequences disclosed may be useful for gene therapy. The fusion
CC protein is useful for preparing a composition for treating a disease or
CC disease symptom in a patient for example septic shock, endotoxic shock,
CC cachexia syndromes associated with bacterial, viral or parasitic
CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
CC associated with treatment for preventing graft rejection. The present
CC sequence is that of a CDR 2 peptide which was used in the exemplification
XX of the invention.
XX
SQ Sequence 17 AA;
Query Match 92.4%; Score 85; DB 8; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 IIYPGSDTRYSPFQG 17
DB 1 IIYPGSDTRYSPFQG 17
Search completed: December 3, 2005, 14:25:05
Job time : 30.0735 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:59 / Search time 4.64898 Seconds
(without alignments)
351.837 Million cell updates/sec

Title: US-10-769-144-14

Perfect score: 92

Sequence: 1 IYFGDSDTYSPSFQ 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	92.4	98	PH1274	Ig heavy chain V r
2	85	92.4	98	S26907	Ig heavy chain V r
3	85	92.4	101	S12428	Ig heavy chain V r
4	85	92.4	101	S12424	Ig heavy chain V r
5	85	92.4	102	PH1266	Ig heavy chain V r
6	85	92.4	102	PH1279	Ig heavy chain V r
7	85	92.4	102	PH1281	Ig heavy chain V r
8	85	92.4	102	PH1277	Ig heavy chain V r
9	85	92.4	102	PH1244	Ig heavy chain V r
10	85	92.4	102	PH1267	Ig heavy chain V r
11	85	92.4	102	PH1272	Ig heavy chain V r
12	85	92.4	102	PH1282	Ig heavy chain V r
13	85	92.4	102	PH1248	Ig heavy chain V r
14	85	92.4	102	PH1280	Ig heavy chain V r
15	85	92.4	102	PH1258	Ig heavy chain V r
16	85	92.4	102	PH1264	Ig heavy chain V r
17	85	92.4	102	PH1259	Ig heavy chain V r
18	85	92.4	102	PH1273	Ig heavy chain V r
19	85	92.4	102	PH1249	Ig heavy chain V r
20	85	92.4	102	PH1271	Ig heavy chain V r
21	85	92.4	102	PH1278	Ig heavy chain V r
22	85	92.4	104	B36006	Ig heavy chain V r
23	85	92.4	113	PH1428	Ig heavy chain V r
24	85	92.4	115	PH1557	Ig heavy chain V r
25	85	92.4	117	A28846	Ig heavy chain pre
26	85	92.4	117	S19670	Ig heavy chain V r
27	85	92.4	123	PH1423	Ig heavy chain V r
28	85	92.4	123	S38492	Ig heavy chain - h
29	85	92.4	123	C36006	Ig heavy chain V r

ALIGNMENTS

RESULT 1

PH1274

Ig heavy chain V region (clone PBL5) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1274

R:Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.

J. Exp. Med. 176, 1073-1081, 1992

A:Title: Extensive and selective mutation of a rearranged VHS gene in human B cell chrom

A:Reference number: PH1232; MUID:93018822; PMID:1402653

A:Accession: PH1274

A:Molecule type: DNA

A:Residues: 1-98 <CAI>

A:Cross-references: UNIPARC:UPI000017683F

A:Experimental source: adult PBL

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 92.4%; Score 85; DB 2; Length 98;

Best Local Similarity 94.1%; Pred. No. 1.3e-06;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGDSDTYSPSFQ 17

Db 54 IYFGDSDTYSPSFQ 70

RESULT 2

S26907

Ig heavy chain V region (DP-73) - human

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26907

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26907

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: UNIPARC:UPI000011641E; EMBL:Z12373; NID:932965; PIDN:CAA78243.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 98;

Best Local Similarity 94.1%; Pred. No. 1.3e-06;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGDSDTYSPSFQ 17

Db 1 IYFGDSDTYSPSFQ 17

Db 50 IYPGDSDTRYSPSQG 66

RESULT 3

S12428
Ig heavy chain V region (5JB) - human
C/Species: Homo sapiens (man)
C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C/Accession: S12428
EMBO J. 8, 3741-3748, 1989
R/Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
A/Title: The smaller human V(H) gene families display remarkably little polymorphism.
A/Reference number: S09421; MUID:90059975; PMID:2511001
A/Accession: S12428
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-101 <SAS>
A/Cross-references: UNIPARC:UPI00001765B; EMBL:X56367
A/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 101;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTRYSPSQG 17

|||||
Db 53 IYPGDSDTRYSPSQG 69

RESULT 4

S12424
Ig heavy chain V region (5) - human
C/Species: Homo sapiens (man)
C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 03-Aug-1998
C/Accession: S12424; S12425; S12426; S12427; S12429; S12432
R/Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A/Title: The smaller human V(H) gene families display remarkably little polymorphism.
A/Reference number: S09421; MUID:90059975; PMID:2511001
A/Accession: S12424

A/Status: preliminary; translation not shown
A/Molecule type: DNA

A/Residues: 1-101 <SAS>

A/Cross-references: UNIPARC:UPI000011636C; EMBL:X56372

A/Experimental source: clones 5AU; 5BLK; 5CH; 5CW; 5LB; 5TT

A/Accession: S12425

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-101 <SA2>

A/Cross-references: UNIPARC:UPI000011636C; EMBL:X56373

A/Accession: S12426

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-101 <SA3>

A/Cross-references: UNIPARC:UPI000011636C; EMBL:X56370

A/Accession: S12427

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-101 <SA4>

A/Cross-references: UNIPARC:UPI000011636C; EMBL:X56368

A/Accession: S12429

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-101 <SA5>

A/Cross-references: UNIPARC:UPI000011636C; EMBL:X56369

A/Accession: S12432

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-101 <SA6>

A/Cross-references: UNIPARC:UPI000011636C; EMBL:X56371

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 101;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTRYSPSQG 17

|||||
Db 53 IYPGDSDTRYSPSQG 69

RESULT 5

PH1266

Ig heavy chain V region (clone VERG5) - human (fragment)
C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PH1266

R/Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.

J. Exp. Med. 176, 1073-1081, 1992

A/Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron

A/Reference number: PH1232; MUID:93018822; PMID:1402653

A/Accession: PH1266

A/Molecule type: mRNA

A/Residues: 1-102 <CAI>

A/Cross-references: UNIPARC:UPI0000176BD2

A/Experimental source: EBV-transformed CD5+ B cell [from adult PBL]

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTRYSPSQG 17

|||||
Db 54 IYPGDSDTRYSPSQG 70

RESULT 6

PH1279

Ig heavy chain V region (clones CLL11, CORD3, CORD4, CORD8, CORD9, CD+1, CD+3, CD+4, CD-

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PH1279

R/Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.

J. Exp. Med. 176, 1073-1081, 1992

A/Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron

A/Reference number: PH1232; MUID:93018822; PMID:1402653

A/Accession: PH1279

A/Molecule type: DNA

A/Residues: 1-102 <CAI>

A/Cross-references: UNIPARC:UPI0000116D01

A/Experimental source: adult PBL

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTRYSPSQG 17

|||||
Db 54 IYPGDSDTRYSPSQG 70

RESULT 7

PH1281

Ig heavy chain V region (clone PBL12) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PH1281
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1281
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Cross-references: UNIPARC:UPI0000176C67
A;Experimental source: adult PBL
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
Db 54 IYPGDSDTYSPSFQ 70

RESULT 8
PH1277
Ig heavy chain V region (clone PBL8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1277
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1277
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Cross-references: UNIPARC:UPI0000176B41
A;Experimental source: adult PBL
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
Db 54 IYPGDSDTYSPSFQ 70

RESULT 9
PH1244
Ig heavy chain V region (clone CORD2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1244
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1244
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Cross-references: UNIPARC:UPI0000176BC8
A;Experimental source: cord blood B cell
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
Db 54 IYPGDSDTYSPSFQ 70

RESULT 10

PH1267
Ig heavy chain V region (clone VERG9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1267
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1267
A;Molecule type: mRNA
A;Residues: 1-102 <CAI>
A;Cross-references: UNIPARC:UPI0000176BD3
A;Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
Db 54 IYPGDSDTYSPSFQ 70

RESULT 11

PH1272
Ig heavy chain V region (clone PBL3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1272
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1272
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Cross-references: UNIPARC:UPI0000176C6C
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSFQ 17
Db 54 IYPGDSDTYSPSFQ 70

RESULT 12

PH1282
Ig heavy chain V region (clone PBL13) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1282
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1282

A:Molecule type: DNA
 A:Residues: 1-102 <CAI>
 A:Cross-references: UNIPARC:UPI0000176C68
 A:Experimental source: adult PBL
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
 Best Local Similarity 94.1%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGSDSTIYSPSFQ 17
 ||||| ||||| ||||| |||||
 Db 54 IIYPGSDTRYSPSFQ 70

RESULT 13
 PH1248
 Ig heavy chain V region (clone CORD6) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PH1248
 R:Cal, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
 J. Exp. Med. 176, 1073-1081, 1992
 A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
 A:Reference number: PH1232; MUID:93018822; PMID:1402653
 A:Accession: PH1248
 A:Molecule type: DNA
 A:Residues: 1-102 <CAI>
 A:Cross-references: UNIPARC:UPI0000176A4E
 A:Experimental source: cord blood B cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
 Best Local Similarity 94.1%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGSDSTIYSPSFQ 17
 ||||| ||||| ||||| |||||
 Db 54 IIYPGSDTRYSPSFQ 70

RESULT 14
 PH1280
 Ig heavy chain V region (clone PBL11) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PH1280
 R:Cal, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
 J. Exp. Med. 176, 1073-1081, 1992
 A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
 A:Reference number: PH1232; MUID:93018822; PMID:1402653
 A:Accession: PH1280
 A:Molecule type: DNA
 A:Residues: 1-102 <CAI>
 A:Cross-references: UNIPARC:UPI0000176B42
 A:Experimental source: adult PBL
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
 Best Local Similarity 94.1%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGSDSTIYSPSFQ 17
 ||||| ||||| ||||| |||||
 Db 54 IIYPGSDTRYSPSFQ 70

RESULT 15

PH1258
 Ig heavy chain V region (clone CD-2) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1258
 R:Cal, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
 J. Exp. Med. 176, 1073-1081, 1992
 A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chron
 A:Reference number: PH1232; MUID:93018822; PMID:1402653
 A:Accession: PH1258
 A:Molecule type: DNA
 A:Residues: 1-102 <CAI>
 A:Cross-references: UNIPARC:UPI0000176BCD
 A:Experimental source: cord blood B cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 85; DB 2; Length 102;
 Best Local Similarity 94.1%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGSDSTIYSPSFQ 17
 ||||| ||||| ||||| |||||
 Db 54 IIYPGSDTRYSPSFQ 70

Search completed: December 3, 2005, 14:33:34
 Job time : 4.64898 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:48 ; Search time 29.9755 Seconds
(without alignments)
400.126 Million cell updates/sec

Title: US-10-769-144-14
Perfect score: 92
Sequence: 1 ILYPGDSDTIYSPSQF 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	65.2	474	Q8R3H6_MOUSE	Q8R3H6 mus musculus
2	59	64.1	118	Q921C4_MOUSE	Q921C4 mus musculus
3	57	62.0	111	Q9D9B8_MOUSE	Q9D9B8 mus musculus
4	56	60.9	483	Q52L53_MOUSE	Q52L51 mus musculus
5	56	60.9	614	Q7TMT6_MOUSE	Q7Tmt6 mus musculus
6	54	58.7	110	Q9JL83_MOUSE	Q9Jl83 mus musculus
7	54	58.7	120	Q5F2I1_MOUSE	Q5f2i1 mus musculus
8	53	57.6	481	Q91WT1_MOUSE	Q91wt1 mus musculus
9	52	56.5	117	HV52_MOUSE	P06327 mus musculus
10	52	56.5	463	Q99LC4_MOUSE	Q99lc4 mus musculus
11	51	55.4	117	HV06_MOUSE	P01750 mus musculus
12	51	55.4	909	Q6WJ05_GOSHI	Q6wj05 gosypium h
13	49	53.3	193	Q4H3H2_CIOIN	Q4h3h2 ciona intes
14	49	53.3	590	Q4V9V8_MOUSE	Q4v9v8 mus musculus
15	49	53.3	860	Q4RR84_TENG	Q4rr84 tetraodon n
16	48	52.2	573	Q6AH99_LEIXX	Q6ah99 leifsonia x
17	48	52.2	958	Q4I5Z0_GIBZE	Q4i5z0 gibberella
18	48	52.2	1216	1 AEGP_RAT	Q63191 rattus norv
19	47	51.1	330	Q93KW0_STRVR	Q93kw0 streptomyce
20	47	51.1	458	Q5B7Z2_RAT	Q5bjz2 rattus norv
21	47	51.1	464	Q6PF95_MOUSE	Q6pf95 mus musculus
22	47	51.1	555	Q5A204_CANAL	Q5a204 candida alb
23	47	51.1	558	Q5A255_CANAL	Q5a255 candida alb
24	47	51.1	567	Q26602_METTH	Q26602 methanobact
25	46	50.0	117	HV05_MOUSE	P01749 mus musculus
26	46	50.0	513	Q5UQP4_MIMIV	Q5uqp4 mimivirus
27	46	50.0	519	Q5BEM2_HUMAN	Q5ebm2 homo sapien
28	46	50.0	537	Q6GNX4_XENLA	Q6gnx4 xenopus lae
29	45	48.9	198	Q5ARM8_EMENI	Q5arm8 aspergillus
30	45	48.9	513	Q52572_PSESP	Q52572 pseudomonas
31	45	48.9	529	Q414V2_GIBZE	Q414v2 gibberella

RESULT 1				
Q8R3H6_MOUSE				
ID	Q8R3H6_MOUSE	PRELIMINARY;	PRT;	474 AA.
AC	Q8R3H6;			
DT	01-JUN-2002	(TrEMBLrel. 21, Created)		
DT	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	Ighg protein.			
CN	Name=Ighg; Synonyms=AU044919;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
EN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=CZECH II;			
RC	TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Pahey J., Helton E., Kettaman M., Madan A.C., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,			
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RC	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=CZECH II;			
RC	TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;			
RA	Director MGC Project;			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC025447; AA025447.1; -, mRNA.			
DR	HSSP; P01869; 1CL7.			
DR	SMR; Q8R3H6; 20-470.			
DR	MGI; MGI:2144967; AU044919.			
DR	MGI; MGI:2144967; Ighg.			
DR	GO; GO:0003823; F:antigen binding; IEA.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig_c1.			
DR	InterPro; IPR003006; Ig_MHC.			

Q4n6s9 theileria p
Q9x224 drosophila
Q54nu3 dictyosteli
P98157 gallus gall
Q925s3 mus musculu
Q6fay3 candida gla
P15110 burkholderi
Q41v17 burkholderi
Q9rvn0 deinococcus
Q61rd1 caenorhabdi
P0a058 staphylococ
P21867 escherichia
Q7ux12 rhodospirill
Q9a5b6 caulobacter

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DR InterPro: IPR003596; Ig v.
DR Pfam: PF07654; CI-set; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 4.
DR PROSITE: PS00290; IG MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 474 AA; 51749 MW; 8608B57C6D2874A CRC64;

Query Match 65.2%; Score 60; DB 2; Length 474;
Best Local Similarity 68.8%; Pred. No. 0.59;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGDSPTIYSPFQ 17
Db 70 IFPGDGDTHYSGKFG 85

RESULT 2
O921C4_MOUSE PRELIMINARY; PRT; 118 AA.
AC O921C4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/C;
RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.A., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Mol. Immunol. 34:441-452(1997).
DR EMBL: U78801; AAD00293.1; -; mRNA.
DR HSRP: P01751; INQB.
DR SMR: O921C4; 1-118.
DR Ensembl: ENSMUSG00000021155; Mus musculus.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; Ig v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90BEC559D31EC4FC CRC64;

Query Match 64.1%; Score 59; DB 2; Length 118;
Best Local Similarity 62.5%; Pred. No. 0.17;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGDSPTIYSPFQ 17
Db 51 IYPGDSPTIYSGKFRG 66

RESULT 3
Q9D9B8_MOUSE PRELIMINARY; PRT; 111 AA.
AC Q9D9B8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:170011011 product:immunoglobulin heavy chain 6 (heavy
DE chain of IgM), full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

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RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nomura R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK007163; BAB24877.1; -, mRNA.
DR HSSP; P01820; 1G7J.
DR SMR; Q9D9B8; 7-106.
DR Ensembl; ENSMUSG0000063520; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;

Query Match 62.0%; Score 57; DB 2; Length 111;
Best Local Similarity 62.5%; Pred. No. 0.34;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGDSPTIYSPSPQ 17
| | | | | | | | | | | | | | | | | |
Db 57 IYPGDDTNYNGKFKG 72

RESULT 4
Q52L51_MOUSE PRELIMINARY; PRT; 483 AA.
AC Q52L51;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RX TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC094065; AAH94065.1; -, mRNA.
DR InterPro; IPR003599; Ig.
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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IGV; 3.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 483 AA; 52167 MW; C0FDB9168795FEB4 CRC64;

Query Match 60.9%; Score 56; DB 2; Length 483;
Best Local Similarity 62.5%; Pred. No. 2.7;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGDSPTIYSPSPQ 17
| | | | | | | | | | | | | | | | | |
Db 70 IYPGDDTNYNGKFKG 85

RESULT 5
Q7TMT6_MOUSE PRELIMINARY; PRT; 614 AA.
AC Q7TMT6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC60843 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053409; AAH53409.1; -, mRNA.
DR HSSP; P01820; 1G7J.
DR Ensembl; ENSMUSG0000054328; Mus musculus.
DR GO; GO:0003823; F-antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 614 AA; 67747 MW; 839BAF3B8D124F89 CRC64;
Query Match 60.9%; Score 56; DB 2; Length 614;
Best Local Similarity 56.2%; Pred. No. 3.5;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IYPGSDTIYSPSQG 17
Db 70 YVPGDGTNYNGKPKG 85

RESULT 6
Q9JL83 MOUSE
ID Q9JL83 MOUSE PRELIMINARY; PRT; 110 AA.
AC Q9JL83;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RX DOI=10.1128/IAI.68.10.5803-5808.2000;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808 (2000).
RL EMBL; AF206023; AAF69321.1; -; mRNA.
DR HSSP; P01751; INQB.
DR SMR; Q9JL83; 1-110.
DR Ensembl; ENSMUSG00000063520; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;
Query Match 58.7%; Score 54; DB 2; Length 110;
Best Local Similarity 56.2%; Pred. No. 1;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 2 IYPGSDTIYSPSQG 17
Db 43 IYPGDDAYNGKPKG 58

RESULT 7
Q5F2I1 MOUSE
ID Q5F2I1 MOUSE PRELIMINARY; PRT; 120 AA.
AC Q5F2I1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Gamma heavy chain variable region (Fragment).
GN Name=IgG1 anti-TS1 VH;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN 1;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN 1;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;

```

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC013490; AAH13490.1; -, mRNA.
DR HSSP; P01751; 1AGW.
DR Ensembl; ENSMUSG000002021155; Mus musculus.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 57.6%; Score 53; DB 2; Length 481;

Best Local Similarity 56.2%; Pred. No. 8.2;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGSDTRIYSPSQG 17
Db 70 IYPGDKTYNEKFKG 85
||||| :|:|:|

RESULT 9

HV52 MOUSE
ID HV52 MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region VH58 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;
RA Manopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
RL Cell 40:271-281(1985).

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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
CC EMBL; M13787; AAA38499.1; -, mRNA.
CC PIR; A02029; HV52A1.
CC HSSP; P01820; 1G7J.
CC SMR; P06327; 20-117.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region VH58 A1/A4.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 56.5%; Score 52; DB 1; Length 117;

Best Local Similarity 56.2%; Pred. No. 2.3;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 2 IYPGSDTRIYSPSQG 17
Db 70 IYPGDKTYNEKFKG 85
||||| :|:|:|

RESULT 10

Q99LC4 MOUSE
ID Q99LC4_MOUSE PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-4 protein.
GN Name=Igh-4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -, mRNA.
DR PIR; B45837; B45837.
DR HSSP; P01869; 1CL7.
DR SMR; Q99LC4; 21-459.
DR MGI; MGI:96446; Igh-4.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0003823; P:antigen binding; IDA.
DR GO; GO:0001973; P:antibacterial humoral response (sensu Verte...; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050762; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type II hypersensit...; IDA.
DR InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
KW Immunoglobulin domain.
SQ SEQUENCE 463 AA; 51008 MW; EAA674C6BBC30783 CRC64;

Query Match 56.5%; Score 52; DB 2; Length 463;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IYPGSDSTIYSPSFOG 17
|||||:|||||:|
Db 70 IYPGSGNTIYSEKFG 85

RESULT 11
ID HV06 MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX MBLINK=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: This germline gene belongs to a set of closely
CC related genes that could encode V regions of NPb antibodies.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A02032; HVMS02.
DR PDB; 1QNZ; NMR; H=21-117.
DR Ensembl; ENSMUSG0000062849; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 102.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Query Match 55.4%; Score 51; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 3.4;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGSDSTIYSPSFOG 17
|:|||||:|:|
Db 70 IYPGSGNTIYSEKFG 85
```

```
Db 70 IHPSDSDTNYNQKFG 85

RESULT 12
Q6WJ05 GOSHI
ID Q6WJ05 GOSHI PRELIMINARY; PRT; 909 AA.
AC Q6WJ05;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Central motor kinesin 1.
DE Name=CKM1;
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lu L., Lee Y.-R.J., Pan R., Liu B.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY283056; AAQ18797.1; -; mRNA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; F:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 909 AA; 100815 MW; 424E3C6DF67EDF4F CRC64;

Query Match 55.4%; Score 51; DB 2; Length 909;
Best Local Similarity 64.3%; Pred. No. 36;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 PGDSDTIYSPSFOG 17
|||||:|||||:|
Db 115 PGTSDGFYSPEFRG 128

RESULT 13
Q4H3H2 CIOIN
ID Q4H3H2 CIOIN PRELIMINARY; PRT; 193 AA.
AC Q4H3H2;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Fringe (Fringe).
DE Name=Ci-Fringe 4;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15269171; DOI=10.1242/dev.01270;
RA Imai K.S., Hino K., Yagi K., Satch N., Satou Y.;
RT "Genomewide surveys of developmentally relevant genes in Ciona
RT intestinalis."
RL Development 131:4047-4058(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE
RX PubMed=12736827; DOI=10.1007/s00427-003-0330-z;
RA Satou Y., Satch N.;
RT "Genomewide surveys of developmentally relevant genes in Ciona
RT intestinalis."
RL Dev. Genes Evol. 213:211-212(2003).
RN [3]
```

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RP NUCLEOTIDE SEQUENCE.
RT "Expressed genes in Ciona intestinalis.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB210450; BAE06455.1; -, mRNA.
FT NON_TER 1
SQ SEQUENCE 193 AA; 22222 MW; B93C2D76BD07D6C2 CRC64;

Query Match 53.3%; Score 49; DB 2; Length 193;
Best Local Similarity 52.9%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Oy 1 IYPGSDSDTIYSPSQFQ 17
Db 27 LIYGGSDVTYPIGKG 43

RESULT 14
Q4V9V8 MOUSE PRELIMINARY; PRT; 590 AA.
AC Q4V9V8
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN Name=Igh-6;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smallos D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC096667; AAH96667.1; -, mRNA.
DR MGI; MGI:96448; Igh-6.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.

KW Hypothetical protein.
SQ SEQUENCE 590 AA; 64892 MW; D425318F9A188B14 CRC64;

Query Match 53.3%; Score 49; DB 2; Length 590;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 2 IYPGSDSDTIYSPSQFQ 17
Db 70 IYPGSGNTYNEKPKG 85

RESULT 15
Q4RR84 TETNG PRELIMINARY; PRT; 860 AA.
AC Q4RR84
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Chromosome 14 SCAF15003, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0030281001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Bottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC Preliminary data.
DR EMBL; CAAS01015003; CAG09098.1; -, Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 860 AA; 95101 MW; 5868355B6346C75 CRC64;

Query Match 53.3%; Score 49; DB 2; Length 860;
Best Local Similarity 61.5%; Pred. No. 71;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 IYPGSDSDTIYSPS 14
Db 278 LHPGDFDVIQSPS 290

Search completed: December 3, 2005, 14:32:24
Job time : 30.9755 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 13:24:58 ; Search time 7.21633 Seconds
(without alignments)
194.765 Million cell updates/sec

Title: US-10-769-144-14

Perfect score: 92
Sequence: 1 IYPCDSPTIYSPFQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RE COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	92.4	98	1	US-08-478-039-81
2	85	92.4	98	1	US-08-476-349A-81
3	85	92.4	98	1	US-08-665-202-33
4	85	92.4	98	2	US-09-315-574-33
5	85	92.4	98	2	US-10-194-975-45
6	85	92.4	111	2	US-09-726-219A-171
7	85	92.4	111	2	US-09-196-522-171
8	85	92.4	117	2	US-08-545-809A-133
9	85	92.4	117	2	US-09-515-697-133
10	85	92.4	119	2	US-09-025-769B-26
11	85	92.4	119	2	US-09-490-070A-26
12	85	92.4	119	2	US-09-490-153-26
13	85	92.4	119	2	US-09-490-324-26
14	85	92.4	120	2	US-09-025-769B-40
15	85	92.4	120	2	US-09-025-769B-67
16	85	92.4	120	2	US-09-490-070A-40
17	85	92.4	120	2	US-09-490-070A-67
18	85	92.4	120	2	US-09-490-153-40
19	85	92.4	120	2	US-09-490-153-67
20	85	92.4	120	2	US-09-490-324-40
21	85	92.4	120	2	US-09-490-324-67
22	84	91.3	125	1	US-08-665-202-56
23	84	91.3	125	2	US-09-315-574-56
24	83	90.2	125	1	US-08-665-202-44
25	83	90.2	125	1	US-08-665-202-45
26	83	90.2	125	1	US-08-665-202-46
27	83	90.2	125	1	US-08-665-202-47

28	83	90.2	125	1	US-08-665-202-48	Sequence 48, Appl
29	83	90.2	125	1	US-08-665-202-49	Sequence 49, Appl
30	83	90.2	125	1	US-08-665-202-50	Sequence 50, Appl
31	83	90.2	125	1	US-08-665-202-51	Sequence 51, Appl
32	83	90.2	125	1	US-08-665-202-52	Sequence 52, Appl
33	83	90.2	125	1	US-08-665-202-53	Sequence 53, Appl
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35	83	90.2	125	1	US-08-665-202-55	Sequence 55, Appl
36	83	90.2	125	1	US-08-665-202-57	Sequence 57, Appl
37	83	90.2	125	1	US-08-665-202-58	Sequence 58, Appl
38	83	90.2	125	2	US-09-315-574-44	Sequence 44, Appl
39	83	90.2	125	2	US-09-315-574-45	Sequence 45, Appl
40	83	90.2	125	2	US-09-315-574-46	Sequence 46, Appl
41	83	90.2	125	2	US-09-315-574-47	Sequence 47, Appl
42	83	90.2	125	2	US-09-315-574-48	Sequence 48, Appl
43	83	90.2	125	2	US-09-315-574-49	Sequence 49, Appl
44	83	90.2	125	2	US-09-315-574-50	Sequence 50, Appl
45	83	90.2	125	2	US-09-315-574-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-08-478-039-81
; Sequence 81, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SNECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant

TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH5 consensus

US-08-476-349A-81

Query Match 92.4%; Score 85; DB 1; Length 98;
Best Local Similarity 94.1%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-08-476-039-81

Query Match 92.4%; Score 85; DB 1; Length 98;
Best Local Similarity 94.1%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTIYSPSFQ 17
Db 50 IIYPGDSDTIYSPSFQ 66

RESULT 2

US-08-476-349A-81
; Sequence 81, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476.349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991

ATTORNEY/AGENT INFORMATION:

NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 81:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

POSITION IN GENOME:

CHROMOSOME/SEGMENT: VH5 consensus

US-08-476-349A-81

Query Match 92.4%; Score 85; DB 1; Length 98;
Best Local Similarity 94.1%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTIYSPSFQ 17
Db 50 IIYPGDSDTIYSPSFQ 66

RESULT 3

US-08-665-202-33
; Sequence 33, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-665-202-33

Query Match 92.4%; Score 85; DB 1; Length 98;
Best Local Similarity 94.1%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTIYSPSFQ 17
Db 50 IIYPGDSDTIYSPSFQ 66

RESULT 4

US-09-315-574-33
; Sequence 33, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:

APPLICANT: Marks, James D.
 APPLICANT: Schizr, Robert
 TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
 TITLE OF INVENTION: Tumor Antigens
 NUMBER OF SEQUENCES: 141
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
 STREET: Four Embarcadero Center, Suite 1100
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-4106
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/315,574
 FILING DATE: 20-MAY-99
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,238
 FILING DATE: 14-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,250
 FILING DATE: 15-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/665,202
 FILING DATE: 13-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 02307E-061411
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 98 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-315-574-33

Query Match 92.4%; Score 85; DB 2; Length 98;
Best Local Similarity 94.1%; Pred. No. 2.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I Y P G D S D T I Y S P S F Q G 17
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p/b 50 I I Y P G D S D T R Y S P S F Q G 66

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RESULT 5
US-10-134-975-45
; Sequence 45, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-194-975-45

Query Match          92.4%   Score 85;   DB 2;   Length 98;
Best Local Similarity 94.1%;   Pred. No. 2.7e-05;
Matches 16;   Conservative 0;   Mismatches 1;   Indels

Qy  1  I I Y P G D S D T T Y S P S F Q G 17
      | | | | | | | | | | | | | | | |
Db  50 I I Y P G D S D T T Y S P S F Q G 66

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RESULT 6
US-09-726-219A-171
; Sequence 171, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members
; FILE REFERENCE: 213639-00013
; CURRENT APPLICATION NUMBER: US/09/726.219A
; CURRENT FILING DATE: 2006-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-171

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Query Match	92.4%	Score 85	DB 2	Length 111
Best Local Similarity	94.1%	Pred. No. 3.1e-05		
Matches 16	Conservative 0	Mismatches 1	Indels 0	Gaps 0

RESULT 7
US-09-196-522-171
; Sequence 171, Application US/09196522

US-10-194-975-45

Query Match	92.4%	Score 85;	DB 2;	Length 98;
Best Local Similarity	94.1%	Pred. No. 2.7e-05;		
Matches 16;	Conservative	0;	Mismatches 1;	Indels

Qy 1 I I Y P G D S D T I Y S P S F Q G 17
| | | | | | | | | | | | | | | | | |
Db 50 I I Y P G D S D T R I Y S P S F Q G 66

RESULT 6
US-09-726-219A-171
; Sequence 171, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A

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; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
; LENGTH: 111
; TYPE: prt
; ORGANISM: Homo sapiens
; US-09-726-219A-171

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Query Match	92.4%	Score 85	DB 2	Length 111
Best Local Similarity	94.1%	Pred. No. 3.1e-05		
Matches 16	Conservative 0	Mismatches 1	Indels 0	Gaps 0

RESULT 7
US-09-196-522-171
; Sequence 171, Application US/09196522

Patent No. 6916605
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clarkson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00004
CURRENT APPLICATION NUMBER: US/09/196,522
CURRENT FILING DATE: 1998-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: Patent in version 3.1
SEQ ID NO 171
LENGTH: 111
TYPE: PRT
ORGANISM: Homo sapiens
US-09-196-522-171

Query Match 92.4%; Score 85; DB 2; Length 111;
Best Local Similarity 94.1%; Pred. No. 3.1e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGSDTIYSPSQ 17
Db 50 IIYPGSDTIYSPSQ 66

RESULT 8
US-08-545-809A-133
Sequence 133, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-133

Query Match 92.4%; Score 85; DB 2; Length 117;
Best Local Similarity 94.1%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGSDTIYSPSQ 17
Db 69 IIYPGSDTIYSPSQ 85

RESULT 9
US-09-515-697-133
Sequence 133, Application US/09515697
Patent No. 6936705
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/515,697
FILING DATE: 29-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809
FILING DATE: 27-MAR-1996
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906

TELEX: 200154
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 133:
US-09-515-697-133

Query Match 92.4%; Score 85; DB 2; Length 117;
Best Local Similarity 94.1%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGSDTIYSPSQG 17
|||||
Db 69 IYFGSDTIYSPSQG 85
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RESULT 10
US-09-025-769B-26
Sequence 26, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-26

Query Match 92.4%; Score 85; DB 2; Length 119;
Best Local Similarity 94.1%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGSDTIYSPSQG 17
|||||
Db 50 IYFGSDTIYSPSQG 66
|||||

RESULT 11
US-09-490-070A-26
Sequence 26, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-070A-26

Query Match 92.4%; Score 85; DB 2; Length 119;
Best Local Similarity 94.1%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYFGSDTIYSPSQG 17
|||||
Db 50 IYFGSDTIYSPSQG 66
|||||

RESULT 12
US-09-490-153-26
Sequence 26, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-153-26
Query Match 92.4%; Score 85; DB 2; Length 119;
Best Local Similarity 94.1%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IIPGSDSTIYSPSQG 17
Db 50 IIPGSDSTIYSPSQG 66
RESULT 13
US-09-490-324-26
; Sequence 26, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324

; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26
Query Match 92.4%; Score 85; DB 2; Length 119;
Best Local Similarity 94.1%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IIPGSDSTIYSPSQG 17
Db 50 IIPGSDSTIYSPSQG 66
RESULT 14
US-09-025-769B-40
; Sequence 40, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-40

Query Match 92.4%; Score 85; DB 2; Length 120;
Best Local Similarity 94.1%; Pred. No. 3.4e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGSDTIYSPSQG 17
|||||
Db 50 IYPGSDTIYSPSQG 66

RESULT 15

US-09-025-769B-67
; Sequence 67, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: US/09/025,769B
; PRIOR APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-67

Query Match 92.4%; Score 85; DB 2; Length 120;
Best Local Similarity 94.1%; Pred. No. 3.4e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGSDTIYSPSQG 17
|||||
Db 50 IYPGSDTIYSPSQG 66

Search completed: December 3, 2005, 14:11:29
Job time : 7.21633 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:27:13 ; Search time 23.3143 Seconds
(without alignments)
304.667 Million cell updates/sec

Title: US-10-769-144-14

Perfect score: 92
Sequence: 1 ILYPGSDTIYSPSQG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	17	5	US-10-769-144-14
2	92	100.0	17	5	US-10-903-191-14
3	92	100.0	116	3	US-09-851-614-4
4	92	100.0	116	4	US-10-035-637-4
5	92	100.0	116	5	US-10-769-144-4
6	92	100.0	116	5	US-10-903-191-4
7	92	100.0	411	5	US-10-769-144-12
8	92	100.0	411	5	US-10-903-191-12
9	92	100.0	468	5	US-10-769-144-2
10	92	100.0	468	5	US-10-903-191-2
11	92	100.0	613	5	US-10-769-144-10
12	92	100.0	613	5	US-10-903-191-10
13	85	92.4	17	4	US-10-384-060-40
14	85	92.4	17	4	US-10-374-932-6
15	85	92.4	17	4	US-10-379-741-6
16	85	92.4	17	4	US-10-128-520-369
17	85	92.4	17	5	US-10-684-957-35
18	85	92.4	17	5	US-10-638-265-95
19	85	92.4	17	5	US-10-726-332-55
20	85	92.4	17	5	US-10-726-332-73
21	85	92.4	17	5	US-10-726-332-88
22	85	92.4	17	5	US-10-726-332-91
23	85	92.4	17	5	US-10-891-658-93
24	85	92.4	17	5	US-10-982-725-6
25	85	92.4	82	4	US-10-078-958-5
26	85	92.4	98	3	US-09-850-165-89
27	85	92.4	98	4	US-10-194-975-45

28	85	92.4	98	4	US-10-125-687-16	Sequence 16, Appl
29	85	92.4	98	4	US-10-041-860-6	Sequence 6, Appl
30	85	92.4	98	4	US-10-041-860-301	Sequence 301, App
31	85	92.4	98	4	US-10-041-860-302	Sequence 302, App
32	85	92.4	98	4	US-10-041-860-312	Sequence 312, App
33	85	92.4	98	4	US-10-041-860-314	Sequence 314, App
34	85	92.4	98	4	US-10-041-860-318	Sequence 318, App
35	85	92.4	98	4	US-10-041-860-320	Sequence 320, App
36	85	92.4	98	4	US-10-041-860-336	Sequence 336, App
37	85	92.4	98	4	US-10-041-860-338	Sequence 338, App
38	85	92.4	98	4	US-10-041-860-367	Sequence 367, App
39	85	92.4	98	4	US-10-308-817-88	Sequence 88, Appl
40	85	92.4	98	4	US-10-032-037B-106	Sequence 106, App
41	85	92.4	98	4	US-10-032-037B-107	Sequence 107, App
42	85	92.4	98	4	US-10-032-037B-108	Sequence 108, App
43	85	92.4	98	4	US-10-029-988B-106	Sequence 106, App
44	85	92.4	98	4	US-10-029-988B-107	Sequence 107, App
45	85	92.4	98	4	US-10-029-988B-108	Sequence 108, App

ALIGNMENTS

RESULT 1
US-10-769-144-14
; Sequence 14, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769.144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-14

Query Match 100.0%; Score 92; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ILYPGSDTIYSPSQG 17
Db 1 ILYPGSDTIYSPSQG 17

RESULT 2
US-10-903-191-14
; Sequence 14, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903.191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979

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; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-14

Query Match      100.0%; Score 92; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIYPGDSDTIYSPSFQ 17
   |||||
Db 1 IIYPGDSDTIYSPSFQ 17

RESULT 3
US-09-851-614-4
; Sequence 4, Application US/09851614
; Publication No. US20030167502A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; FILE REFERENCE: MXI-166
; CURRENT APPLICATION NUMBER: US/09/851,614
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-614-4

Query Match      100.0%; Score 92; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIYPGDSDTIYSPSFQ 17
   |||||
Db 50 IIYPGDSDTIYSPSFQ 66

RESULT 4
US-10-035-637-4
; Sequence 4, Application US/10035637
; Publication No. US20030031667A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035,637
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/851,614
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-4

Query Match      100.0%; Score 92; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIYPGDSDTIYSPSFQ 17
   |||||
Db 50 IIYPGDSDTIYSPSFQ 66

RESULT 5
US-10-769-144-4
; Sequence 4, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-4

Query Match      100.0%; Score 92; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIYPGDSDTIYSPSFQ 17
   |||||
Db 50 IIYPGDSDTIYSPSFQ 66

RESULT 6
US-10-903-191-4
; Sequence 4, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-4

Query Match      100.0%; Score 92; DB 5; Length 116;
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Best Local Similarity 100.0%; Pred. No. 1.3e-06; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Db 191 IIYPGSDTIYSPSFQ 207	
Query 1 IIYPGSDTIYSPSFQ 17 		RESULT 9	
Db 50 IIYPGSDTIYSPSFQ 66 		US-10-769-144-2	
		; Sequence 12, Application US/10769144	
		; Publication No. US20040248215A1	
		; GENERAL INFORMATION:	
		; APPLICANT: Keler, Tibor	
		; APPLICANT: Endres, Michael	
		; APPLICANT: He, Lizhen	
		; APPLICANT: Ramakrishna, Venky	
		; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES	
		; FILE REFERENCE: MXI-301	
		; CURRENT APPLICATION NUMBER: US/10/769,144	
		; CURRENT FILING DATE: 2004-01-30	
		; PRIOR APPLICATION NUMBER: 60/443979	
		; PRIOR FILING DATE: 2003-01-31	
		; NUMBER OF SEQ ID NOS: 32	
		; SOFTWARE: FastSEQ for Windows Version 4.0	
		; SEQ ID NO 12	
		; LENGTH: 411	
		; TYPE: PRT	
		; ORGANISM: Homo sapiens	
		US-10-769-144-12	
Query Match 100.0%; Score 92; DB 5; Length 411;		Query Match 100.0%; Score 92; DB 5; Length 468;	
Best Local Similarity 100.0%; Pred. No. 5.4e-06;		Best Local Similarity 100.0%; Pred. No. 6.2e-06;	
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Query 1 IIYPGSDTIYSPSFQ 17 		Query 1 IIYPGSDTIYSPSFQ 17 	
Db 191 IIYPGSDTIYSPSFQ 207 		Db 69 IIYPGSDTIYSPSFQ 85 	
		RESULT 10	
		US-10-903-191-2	
		; Sequence 2, Application US/10903191	
		; Publication No. US20050180983A1	
		; GENERAL INFORMATION:	
		; APPLICANT: Keler, Tibor	
		; APPLICANT: Endres, Michael	
		; APPLICANT: He, Lizhen	
		; APPLICANT: Ramakrishna, Venky	
		; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES	
		; FILE REFERENCE: MXI-301CP	
		; CURRENT APPLICATION NUMBER: US/10/903,191	
		; CURRENT FILING DATE: 2004-07-30	
		; PRIOR APPLICATION NUMBER: 10/769144	
		; PRIOR FILING DATE: 2004-01-30	
		; PRIOR APPLICATION NUMBER: 60/443979	
		; PRIOR FILING DATE: 2003-01-31	
		; NUMBER OF SEQ ID NOS: 32	
		; SOFTWARE: FastSEQ for Windows Version 4.0	
		; SEQ ID NO 2	
		; LENGTH: 468	
		; TYPE: PRT	
		; ORGANISM: Homo sapiens	
		US-10-903-191-2	
Query Match 100.0%; Score 92; DB 5; Length 411;		Query Match 100.0%; Score 92; DB 5; Length 468;	
Best Local Similarity 100.0%; Pred. No. 5.4e-06;		Best Local Similarity 100.0%; Pred. No. 6.2e-06;	
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Query 1 IIYPGSDTIYSPSFQ 17 		Query 1 IIYPGSDTIYSPSFQ 17 	
Db 191 IIYPGSDTIYSPSFQ 12 		Db 69 IIYPGSDTIYSPSFQ 85 	
		RESULT 11	
		US-10-769-144-10	

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; Sequence 10, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: VH CDR2 sequence
US-10-769-144-10

Query Match      100.0%; Score 92; DB 5; Length 613;
Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 I I Y P G S D T I Y S P S F Q G 17
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Db 69 I I Y P G S D T I Y S P S F Q G 85

RESULT 12
US-10-903-191-10
; Sequence 10, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-10

Query Match      100.0%; Score 92; DB 5; Length 613;
Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 I I Y P G S D T I Y S P S F Q G 17
   ||||| ||||| ||||| |||||
Db 69 I I Y P G S D T I Y S P S F Q G 85

RESULT 13
US-10-384-060-40
; Sequence 40, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: S4710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VH CDR2 sequence
US-10-384-060-40

Query Match      92.4%; Score 85; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I Y P G S D T I Y S P S F Q G 17
   ||||| ||||| ||||| |||||
Db 1 I I Y P G S D T I Y S P S F Q G 17

RESULT 14
US-10-374-932-6
; Sequence 6, Application US/10374932
; Publication No. US20030235586A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus Antonius
; APPLICANT: Schuurman, Janine
; APPLICANT: Gerritsen, Arnout F.
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Petersen, Jorgen
; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
; FILE REFERENCE: GMI-024CP
; CURRENT APPLICATION NUMBER: US/10/374,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 10/226615
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-932-6

Query Match      92.4%; Score 85; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 I I Y P G S D T I Y S P S F Q G 17
   ||||| ||||| ||||| |||||
Db 1 I I Y P G S D T I Y S P S F Q G 17

RESULT 15
US-10-379-741-6
; Sequence 6, Application US/10379741
; Publication No. US20040071702A1
; GENERAL INFORMATION:
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; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus Antonius
; APPLICANT: Schuurman, Janine
; APPLICANT: Gerritsen, Arnout F.
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Petersen, Jorgen
; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
; FILE REFERENCE: GMI-024CP2
; CURRENT APPLICATION NUMBER: US/10/379,741
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 10/226615
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-741-6

Query Match          92.4%; Score 85; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IIYPGDSDTIYSPSFQG 17
   |||||
Db 1 IIYPGDSDTIYSPSFQG 17
   |||||

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Job time : 24.3143 secs
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-10-769-144-14
Perfect score: 92
Sequence: 1 IYPGDSDTIYSPSQ 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	85	92.4	98	7	US-11-054-669-45
2	85	92.4	98	7	US-11-084-554-56
3	85	92.4	252	7	US-11-054-515-1537
4	81	88.0	248	7	US-11-054-515-1995
5	80	87.0	249	7	US-11-054-515-1312
6	77	83.7	248	7	US-11-054-515-1
7	69	75.0	249	7	US-11-054-515-1957
8	61	66.3	119	7	US-11-054-669-124
9	58	63.0	248	6	US-10-512-184-36
10	58	63.0	615	6	US-10-512-184-50
11	57	62.0	17	6	US-10-502-145-27
12	57	62.0	121	6	US-10-502-145-21
13	57	62.0	247	7	US-11-084-717-21
14	57	62.0	543	6	US-10-495-664-3
15	56	60.9	248	7	US-11-054-515-2088
16	55	59.8	251	7	US-11-054-515-1390
17	54	58.7	247	7	US-11-084-717-23
18	54	58.7	247	7	US-11-084-717-25
19	53	57.6	247	7	US-11-054-515-2103
20	51	55.4	249	7	US-11-054-515-1970
21	48	52.2	17	6	US-10-839-799-116
22	48	52.2	98	7	US-11-054-669-11
23	48	52.2	117	6	US-10-839-799-132
24	48	52.2	125	7	US-11-096-074-58
25	48	52.2	136	6	US-10-839-799-29

26	48	52.2	136	6	US-10-839-799-99	Sequence 99, Appl
27	48	52.2	269	6	US-10-839-799-109	Sequence 109, Appl
28	47	51.1	117	6	US-10-932-334-76	Sequence 76, Appl
29	47	51.1	118	6	US-10-507-662-35	Sequence 35, Appl
30	46	50.0	98	7	US-11-054-669-5	Sequence 5, Appl
31	46	50.0	98	7	US-11-084-554-17	Sequence 17, Appl
32	46	50.0	118	6	US-10-507-662-34	Sequence 34, Appl
33	45	48.9	119	6	US-11-054-669-123	Sequence 123, Appl
34	45	48.9	119	7	US-11-054-515-1895	Sequence 1895, Appl
35	45	48.9	253	7	US-11-054-515-2098	Sequence 2098, Appl
36	45	48.9	253	7	US-11-054-515-1001	Sequence 1001, Appl
37	45	48.9	254	7	US-11-054-515-1334	Sequence 1334, Appl
38	45	48.9	254	7	US-11-054-515-3240	Sequence 3240, Appl
39	44	47.8	247	7	US-11-054-515-1952	Sequence 1952, Appl
40	44	47.8	250	7	US-11-054-515-1084	Sequence 1084, Appl
41	44	47.8	251	7	US-11-054-515-1951	Sequence 1951, Appl
42	44	47.8	253	7	US-11-054-515-2101	Sequence 2101, Appl
43	44	47.8	253	7	US-11-054-515-153	Sequence 153, Appl
44	44	47.8	472	6	US-10-485-517-153	Sequence 153, Appl
45	43	46.7	119	6	US-10-477-950-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-11-054-669-45
; Sequence 45, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-45

Query Match 92.4%; Score 85; DB 7; Length 98;
Best Local Similarity 94.1%; Pred. NO. 9.8e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSQ 17
Db 50 IYPGDSDTIYSPSQ 66

RESULT 2
US-11-084-554-56
; Sequence 56, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Larry L.
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENTX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24

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; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-56

Query Match          92.4%; Score 85; DB 7; Length 98;
Best Local Similarity 94.1%; Pred. No. 9.8e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IYPGDSDTIYSPSFQ 17
        |||||:|||||
Db      50 IYPGDSDTIYSPSFQ 66

RESULT 3
US-11-054-515-1537
; Sequence 1537, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1537
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1537

Query Match          92.4%; Score 85; DB 7; Length 252;
Best Local Similarity 94.1%; Pred. No. 2.6e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IYPGDSDTIYSPSFQ 17
        |||||:|||||
Db      50 IYPGDSDTIYSPSFQ 66

RESULT 4
US-11-054-515-1995
; Sequence 1995, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
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; ORGANISM: Homo sapiens
US-11-054-515-1312
Query Match      87.0%; Score 80; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 1.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSQF 17
    |||||:|||||
Db 50 IYPGDSNTRYSPSQF 66

RESULT 6
US-11-054-515-1
; Sequence 1, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1957
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1957

Query Match      75.0%; Score 69; DB 7; Length 249;
Best Local Similarity 76.5%; Pred. No. 0.0001;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IYPGDSDTIYSPSQF 17
    |||||:|||||
Db 50 IYPPDSDTYRPSFQ 66

RESULT 8
US-11-054-669-124
; Sequence 124, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 124
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-124

Query Match      66.3%; Score 61; DB 7; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.00096;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IYPGDSDTIYSPSQF 17
    |||||:|||||
Db 51 IYPRSGDTSYNPSFQ 66

RESULT 9
US-10-512-184-36
; Sequence 36, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
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; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 36
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: specificity against S
; OTHER INFORMATION: originates from Mus m
US-10-512-184-36

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Query Match 63.0%; Score 58; DB 6; Length 248;
Best Local Similarity 62.5%; Pred. No. 0.0064;
Matches 10; Conservative 3; Mismatches 3; Indels

Qy 2 YPGDSDTIYSPSQG 17
|||:||||:|:
Db 53 YPGNSDTSYNQKFKG 68

RESULT 10
US-10-512-184-50
; Sequence 50, Application US/10512184

/ GENERAL INFORMATION:
 / APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
 / TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
 / TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
 / TITLE OF INVENTION: resistance against fungi

Query Match 63.0%; Score 58; DB 6; Length 615;
Best Local Similarity 62.5%; Pred. No. 0.017;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IYPGDSDTIYSPSQG 17
|||:||||:|:
Db 394 IYPCGSDTSYNOKFKG 409

```

RESULT 11
US-10-502-145-27
/ Sequence 27, Application US/10502145
/ Publication No. US2005024406A1
/ GENERAL INFORMATION:
/ APPLICANT: MACKAY, CHARLES REAY
/ TITLE OF INVENTION: Anti-C5aR antibodies
/ FILE REFERENCE: RICE-032
/ CURRENT APPLICATION NUMBER: US/10/502,145
/ CURRENT FILING DATE: 2004-07-19
/ PRIOR APPLICATION NUMBER: USSN 60/350,961
/ PRIOR FILING DATE: 2002-01-25
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 27
/ LENGTH: 17
/

```

; TYPE: PRT
; ORGANISM: Mus musculus
US-10-502-145-27

Query Match 62.0%; Score 57; DB 6; Length 17;
Best Local Similarity 62.5%; Pred. No. 0.00056;
Matches 10; Conservative 2; Mismatches 4; Indels

Qy 2 IYPGDSDTIYSPSQG 17
||| | | : | |
Db 2 IYPGDGDTKYNGKFXG 17

```

RESULT 12
US-10-502-145-21
; Sequence 21, Application US/10502145
; Publication No. US20050244406A1
; GENERAL INFORMATION:
; APPLICANT: MACKAY, CHARLES REAY
; TITLE OF INVENTION: Anti-C5ar antibodies and uses thereof
; FILE REFERENCE: RICE-032
; CURRENT APPLICATION NUMBER: US/10/502,145
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: USSN 60/350,961
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-502-145-21

```

Query Match 62.0%; Score 57; DB 6; Length 121;
Best Local Similarity 62.5%; Pred. No. 0.0044;
Matches 10; Conservative 2; Mismatches 4; Indels

Qy 2 IYPGDSDTIYSPSQG 17
||| ||| : ||
Db 51 IYPGDGDTKYNGKFKG 66

```

RESULT 13
US-11-084-717-21
; Sequence 21, Application US/11084717
; Publication No. US20050260736A1
; GENERAL INFORMATION:
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: JEONG, KI-JUN
; APPLICANT: HARVEY, BARRETT R.
; APPLICANT: IYERSON, BRENT L.
; TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES
; FILE REFERENCE: UTSB:723JUS
; CURRENT APPLICATION NUMBER: US/11/084,717
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/554,324
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: 10/620,278
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,058
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-084-717-21

```

Query Match 62.0%; Score 57; DB 7; Length 247;


```
Best Local Similarity 62.5%; Pred. No. 0.0092;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGDSDTIYSPSQ 17
    ||||| ||| |. |. |. |
Db 179 IYPGDDTNYNGKFKG 194

RESULT 14
US-10-495-664-3
; Sequence 3, Application US/10495664
; Publication No. US2005024416A1
; GENERAL INFORMATION:
; APPLICANT: JUNG, GUNDRAM
; TITLE OF INVENTION: BISPECIFIC ANTI-CD28 ANTIBODY MOLECULE
; FILE REFERENCE: 034258-0801
; CURRENT APPLICATION NUMBER: US/10/495,664
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: PCT/EP02/12545
; PRIOR FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: DE 101 56 482.1
; PRIOR FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 3
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: protein construct
US-10-495-664-3

Query Match 62.0%; Score 57; DB 6; Length 543;
Best Local Similarity 62.5%; Pred. No. 0.021;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGDSDTIYSPSQ 17
    ||||| ||| |. |. |
Db 337 IYPGDDTNYNGKFKG 352

RESULT 15
US-11-054-515-2088
; Sequence 2088, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2088
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2088

Query Match 60.9%; Score 56; DB 7; Length 248;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGDSDTIYSPSQ 17
    ||||| ||| |. |. |
Db 51 IDPSDSTNYSPSQ 66

Search completed: December 3, 2005, 14:17:55
Job time : 1.97143 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 14:10:00 ; Search time 198.384 Seconds
(without alignments)
256.916 Million cell updates/sec

Title: US-10-769-144-4

Perfect score: 621

Sequence: 1 EVQLVQSGAEVKPGESLR.....TRGDRGVYMGQGLTVTVSS 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	621	100.0	116	5	AAM48005 Human mon
2	621	100.0	116	8	ADR46821 Human ant
3	621	100.0	411	8	ADR46829 Human pB1
4	621	100.0	468	8	ADR46819 Human ant
5	621	100.0	613	8	ADR46827 Human bet
6	560	90.2	117	8	ADP47223 Human pho
7	558.5	89.9	245	4	AAB67622 Human leu
8	558	89.9	117	8	ADP47094 Human pho
9	556	89.5	120	2	AAP27555 Human ab
10	556	89.5	120	6	ABJ18677 Antibody
11	556	89.5	120	6	ABJ18720 Antibody
12	552.5	89.0	252	5	ABP45526 Human Bly
13	552.5	89.0	252	7	ADG96353 Single ch
14	552.5	89.0	266	8	ADP69305 Human lun
15	552	88.9	117	8	ADP47229 Human pho
16	550.5	88.6	118	8	ADP47230 Human pho
17	550	88.6	224	6	ABR01533 Human ant
18	550	88.6	224	6	ABR01530 Human ant
19	550	88.6	226	6	ABR01522 Human ant
20	549.5	88.5	474	9	AEa12652 Heavy cha
21	549.5	88.5	474	9	AEa12653 Heavy cha
22	549.5	88.5	474	9	AEa18909 Variant h
23	549.5	88.5	474	9	AEa18908 Heavy cha
24	549.5	88.5	474	9	AEa18548 Heavy cha

25	549.5	88.5	474	9	AEa18549 Variant O
26	549.5	88.5	474	9	AEa10642 Human ant
27	549.5	88.5	474	9	AEa10641 Human ant
28	548.5	88.3	118	8	ADP47116 Human pho
29	548.5	88.3	118	8	ADP47219 Human pho
30	548.5	88.3	138	6	AAE37207 Human AB-
31	548.5	88.3	138	9	AEa16229 Anti-huma
32	548.5	88.3	245	4	AAB67621 Human leu
33	548	88.2	117	8	ADL70771 Anti-TNPa
34	548	88.2	224	6	ABR01528 Human ant
35	547	88.1	224	6	ABR01545 Human ant
36	546.5	88.0	118	8	ADP47098 Human pho
37	546.5	88.0	118	8	ADP47114 Human pho
38	546.5	88.0	118	8	ADP47092 Human pho
39	546.5	88.0	118	8	ADP47224 Human pho
40	546.5	88.0	119	9	ADZ42024 Ig H chai
41	545.5	87.8	118	8	ADP47228 Human pho
42	545	87.8	116	8	ADP22260 Human ant
43	544	87.6	116	8	ADP22194 Human ant
44	544	87.6	126	7	ADK18889 Anti-huma
45	544	87.6	224	6	ABR01527 Human ant

ALIGNMENTS

RESULT 1	
AAM48005	
ID AAM48005 standard; protein; 116 AA.	
XX	
AC AAM48005;	
XX	
DT 08-MAR-2002 (first entry)	
XX	
DE Human monoclonal antibody B11 variable heavy chain protein.	
XX	
KW Human; monoclonal antibody; B11; antigen binding portion; dendritic cell;	
KW mannose receptor; growth; cytolysis; pathogen; virus; bacterium;	
KW autoimmune disease; inflammatory disorder; rheumatoid arthritis;	
KW multiple sclerosis; diabetes mellitus; immunomodulatory;	
KW antiinflammatory; antirheumatic; antiarthritic; neuroprotective;	
KW antidabetic; anianaemic; endocrine; dermatological; antithyroid;	
KW uropathic; ophthalmological; muscular.	
XX	
OS Homo sapiens.	
XX	
PN WO200185798-A2.	
XX	
PD 15-NOV-2001.	
XX	
PF 08-MAY-2001; 2001WO-US015114.	
XX	
PR 08-MAY-2000; 2000US-0203126P.	
PR 07-SEP-2000; 2000US-0230739P.	
XX	
PA (MEDA-) MEDAREX INC.	
XX	
PI Deo YM, Keler T;	
XX	
DR WPI; 2002-089788/12.	
DR N-PSDB; ABA05500.	
XX	
PT New human monoclonal antibodies specific for dendritic cells, useful for	
PT inhibiting growth or inducing cytolysis of a dendritic cell and treating	
PT or preventing a dendritic cell mediated disease, e.g., autoimmune	
disorders.	
XX	
PS Example 2; Fig 13; 95pp; English.	
XX	
CC The invention relates to human monoclonal antibodies or their antigen	
CC binding portions that specifically bind to dendritic cells and has one or	
CC more of the following characteristics: (a) a binding affinity constant to	
CC a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability	

T cell-mediated immune response; immunisation; cytostatic; antimicrobial; immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial; CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease; melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes; antibody B11; pB11-betahCG molecular conjugate; fusion protein.

Homo sapiens.
Synthetic.

WO2004074432-A2.
02-SEP-2004.
30-JAN-2004; 2004WO-US002725.
31-JAN-2003; 2003US-0443979P.
(MEDA-) MEDAREX INC.

Keler T, Endres M, He L, Ramakrishna V;
WPI: 2004-635555/61.
N-PSDB; ADR46828.

New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.

Claim 16; SEQ ID NO 12; 82pp; English.

The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VHS-51 or Vκ-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to betahCG, where the chain antibody that binds to human APCs linked to betahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen, comprising forming a conjugate of the antigen and a monoclonal antibody which binds to APCs, and contacting the conjugate either in vivo or ex vivo with APCs such that the antigen is internalised, processed and presented to T cells in a manner which induces or enhances a cytotoxic T cell response against the antigen. The molecular conjugate has cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic, virucide and antimalarial activities, and can be used as a CD8 agonist, and in vaccines. The methods and compositions of the present invention are useful for inducing a cytotoxic T cell response, and in particular for treating autoimmune disorders, cancers and infectious diseases by eliciting a potent antigen-specific cytotoxic T lymphocyte response, including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and herpes. The present sequence represents a human pB11-betahCG molecular conjugate, which is used in the exemplification of the present invention.

Sequence 411 AA;

Query Match 100.0%; Score 621; DB 8; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.7e-49;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLRISCKGSGSFSTYYTIGWVRQMPGKGLEWGIYPGDSDTIY 60
Db 142 EVQLVQSGAEVKKPGESLRISCKGSGSFSTYYTIGWVRQMPGKGLEWGIYPGDSDTIY 201
QY 61 SPSPQGOVTTISADKSIISTAYLQWSSSLKASDPTAMYYCTRGDGVGYWGQGLTVTVSS 116
Db 202 SPSPQGOVTTISADKSIISTAYLQWSSSLKASDPTAMYYCTRGDGVGYWGQGLTVTVSS 257

RESULT 4
ADR46819
ID ADR46819 standard; protein; 468 AA.
XX AC ADR46819;
XX DT 18-NOV-2004 (first entry)
XX DE Human antibody B11 heavy chain variable region protein SEQ ID NO:2.
XX KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW betahCG; beta chorionic gonadotropin; antibody;
KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW antibody B11; heavy chain variable region.
XX OS Homo sapiens.
XX FN WO2004074432-A2.
XX PD 02-SEP-2004.
XX PF 30-JAN-2004; 2004WO-US002725.
XX PR 31-JAN-2003; 2003US-0443979P.
XX PA (MEDA-) MEDAREX INC.
XX PI Keler T, Endres M, He L, Ramakrishna V;
XX WPI: 2004-635555/61.
XX DR N-PSDB; ADR46818.
XX PS New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.
XX PT Claim 13; SEQ ID NO 2; 82pp; English.
XX CC The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (betahCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VHS-51 or Vκ-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betahCG; (2) a molecular conjugate comprising a human single chain antibody that binds to human APCs linked to betahCG, where the chain antibody that binds to human APCs linked to betahCG, where the conjugate comprises the 411 amino acid sequence of SEQ ID NO:12 (ADR46829); (3) a composition comprising any of the molecular conjugates as described above, and a carrier, optionally in combination with an adjuvant; (4) inducing or enhancing a T cell-mediated immune response, against betahCG, comprising contacting any of the molecular conjugates described above with APCs such that the antigen is processed and presented to T cells in a manner which induces or enhances a T cell-mediated response against the antigen; (5) immunising a subject comprising administering any of the molecular conjugates described above, optionally in combination with an adjuvant, a cytokine which stimulates proliferation of dendritic cells and/or an immunostimulatory agent; and (6) inducing or enhancing a cytotoxic T cell response against an antigen,

```
CC comprising forming a conjugate of the antigen and a monoclonal antibody
CC which binds to APCs, and contacting the conjugate either in vivo or ex
CC vivo with APCs such that the antigen is internalised, processed and
CC presented to T cells in a manner which induces or enhances a cytotoxic T
CC cell response against the antigen. The molecular conjugate has
CC cytototoxic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC virucide and antimalarial activities, and can be used as a CD8 agonist,
CC and in vaccines. The methods and compositions of the present invention
CC are useful for inducing a cytotoxic T cell response, and in particular
CC for treating autoimmune disorders, cancers and infectious diseases by
CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC herpes. The present sequence represents a human antibody B11 heavy chain
CC variable region, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 468 AA;
  Query Match          100.0%; Score 621; DB 8; Length 468;
  Best Local Similarity 100.0%; Pred. No. 3.1e-49;
  Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYTWIGVQRMPKGLWNGIIPGDSDTIY 60
Db 20 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYTWIGVQRMPKGLWNGIIPGDSDTIY 79
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVDPYWGQGLTVTVSS 116
Db 80 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVDPYWGQGLTVTVSS 135

RESULT 5
ADR46827
ID ADR46827 standard; protein; 613 AA.
XX
AC ADR46827;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human betahCG-B11 molecular conjugate protein SEQ ID NO:10.
XX
KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW betahCG; beta chorionic gonadotropin; antibody;
KW T cell-mediated immune response; immunisation; cytototoxic; antimicrobial;
KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW antibody B11; betahCG-B11 molecular conjugate; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004074432-A2.
XX
PD 02-SEP-2004.
XX
PF 30-JAN-2004; 2004WO-US002725.
XX
PR 31-JAN-2003; 2003US-0443979P.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Keler T, Endres M, He L, Ramakrishna V;
XX
DR WPI; 2004-635555/61.
DR N-PSDB; ADR46826.
XX
FT New molecular conjugate having a monoclonal antibody that binds to human
FT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
FT cytotoxic T cell response in cancers and infectious diseases.
XX
PB Example 1; SEQ ID NO 10; 82pp; English.
```

```
XX The present invention describes a molecular conjugate comprising a
CC monoclonal antibody that binds to human antigen presenting cells (APCs)
CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC comprises a heavy and/or light chain variable region derived from a human
CC VH5-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences
CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
CC described: (1) a molecular conjugate comprising a human antibody heavy
CC chain and a human antibody light chain, where either or both chains are
CC linked to betahCG; (2) a molecular conjugate comprising a human single
CC chain antibody that binds to human APCs linked to betahCG, where the
CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC (ADR46829); (3) a composition comprising any of the molecular conjugates
CC as described above, and a carrier, optionally in combination with an
CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC against betahCG, comprising contacting any of the molecular conjugates
CC described above with APCs such that the antigen is processed and
CC presented to T cells in a manner which induces or enhances a T cell-
CC mediated response against the antigen; (5) immunising a subject
CC comprising administering any of the molecular conjugates described above,
CC optionally in combination with an adjuvant, a cytokine which stimulates
CC proliferation of dendritic cells and/or an immunostimulatory agent; and
CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC comprising forming a conjugate of the antigen and a monoclonal antibody
CC which binds to APCs, and contacting the conjugate either in vivo or ex
CC vivo with APCs such that the antigen is internalised, processed and
CC presented to T cells in a manner which induces or enhances a cytotoxic T
CC cell response against the antigen. The molecular conjugate has
CC cytototoxic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC virucide and antimalarial activities, and can be used as a CD8 agonist,
CC and in vaccines. The methods and compositions of the present invention
CC are useful for inducing a cytotoxic T cell response, and in particular
CC for treating autoimmune disorders, cancers and infectious diseases by
CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC herpes. The present sequence represents a human betahCG-B11 molecular
CC conjugate, which is used in the exemplification of the present invention.
XX
SQ Sequence 613 AA;
  Query Match          100.0%; Score 621; DB 8; Length 613;
  Best Local Similarity 100.0%; Pred. No. 4.1e-49;
  Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYTWIGVQRMPKGLWNGIIPGDSDTIY 60
Db 20 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYTWIGVQRMPKGLWNGIIPGDSDTIY 79
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVDPYWGQGLTVTVSS 116
Db 80 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVDPYWGQGLTVTVSS 135

RESULT 6
ADP47223
ID ADP47223 standard; protein; 117 AA.
XX
AC ADP47223;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human phospholipase A2-specific monoclonal antibody heavy chain #21.
XX
KW human; monoclonal antibody; phospholipase A2; PLA2;
KW inflammatory disorder; degenerative disorder;
KW joint inflammatory reaction; skin inflammatory reaction;
KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS Homo sapiens.
XX
PN WO2004050850-A2.
XX
```

PD 17-JUN-2004.
XX
XX 02-DEC-2003; 2003WO-US038234.
XX
XX
XX 02-DEC-2002; 2002US-0430724P.
XX
XX (ABGE-) AGENIX INC.
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
XX Jia X, Nocerini MR;
XX WPI; 2004-461119/43.
XX
XX New human monoclonal antibody that binds to phospholipase A2 (PLA2),
XX useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
XX asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
XX Example 5; SEQ ID NO 139; 128pp; English.
XX
XX The invention comprises a human monoclonal antibody that binds to
XX phospholipase A2 (PLA2). The monoclonal antibody of the invention is
XX useful in the preparation of a medicament for the treatment of
XX inflammatory and degenerative disorders stemming from inflammatory
XX reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
XX asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
XX amino acid sequence represents the heavy chain from a monoclonal antibody
XX that is specific for the human phospholipase A2 (PLA2) enzyme.
XX
XX Sequence 117 AA;
SQ

Query Match 90.2%; Score 560; DB 8; Length 117;
Best Local Similarity 91.4%; Pred. No. 3.3e-44;
Matches 106; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGDSFTTYYWGVRQMPGKGLEWMGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGDSFTTYYWGVRQMPGKGLEWMGIIYPGDSDTIY 60
Qy 61 SPSPFGQVTTISADKSIISTAYLQWSSLKASDTAMYCYTRGDRGVYWGQGLTLVTSS 116
Db 61 SPSPFGQVTTISADKSIISTAYLQWSSLKASDTAMYCYTRGDRGVYWGQGLTLVTSS 116

RESULT 7
AAB67622
ID AAB67622 standard; protein; 245 AA.
XX
XX AAB67622;
XX
XX 29-MAY-2001 (first entry)
XX
XX Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_6.
XX
XX Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
XX miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
XX
XX Homo sapiens.
XX
XX WO200114558-A1.
XX
XX 01-MAR-2001.
XX
XX 28-AUG-2000; 2000WO-EP008388.
XX
XX 26-AUG-1999; 99EP-00116691.
XX
XX (MORP-) MORPHOSYS AG.
XX
XX Kretzschmar T, Tesar M, Marget M, Kroenke M;
XX WPI; 2001-218451/22.
XX

PT Novel isolated human immunoglobulin or functional immunoglobulin fragment
PT specific for human leukocyte antigen Cw6, useful for treatment of humans
XX and for human leukocyte antigen phenotyping.
XX
XX Claim 3; Fig 1; 23pp; English.
XX
XX AAB67617-23 represent single chain antibody (scFv) fragments which are
XX specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived
XX from a synthetic human combinatorial antibody library based on molecular
XX consensus frameworks and CDRs randomised with trinucleotides. The
XX specification describes a human immunoglobulin fragments specific for HLA
XX -Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of
XX natural killer cell silencing as well as miscarriages. HLA-Cw6
XX demonstrates a disequilibrium in some recurrent abortions. Psoriasis may
XX also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are
XX useful for the preparation of a pharmaceutical for the treatment of
XX humans. They are also useful for HLA phenotyping
XX
XX Sequence 245 AA;
SQ

Query Match 89.9%; Score 558.5; DB 4; Length 245;
Best Local Similarity 91.5%; Pred. No. 1e-43;
Matches 107; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGDSFTTYYWGVRQMPGKGLEWMGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGDSFTTYYWGVRQMPGKGLEWMGIIYPGDSDTIY 60
Qy 61 SPSPFGQVTTISADKSIISTAYLQWSSLKASDTAMYCYTRGD-RGVYWGQGLTLVTSS 116
Db 61 SPSPFGQVTTISADKSIISTAYLQWSSLKASDTAMYCYTRGD-RGVYWGQGLTLVTSS 117

RESULT 8
ADP47094
ID ADP47094 standard; protein; 117 AA.
XX
XX ADP47094;
XX
XX 09-SEP-2004 (first entry)
XX
XX Human phospholipase A2-specific monoclonal antibody heavy chain #4.
XX
XX human; monoclonal antibody; phospholipase A2; PLA2;
XX inflammatory disorder; degenerative disorder;
XX joint inflammatory reaction; skin inflammatory reaction;
XX blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
XX Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
XX Homo sapiens.
XX
XX WO2004050850-A2.
XX
XX 17-JUN-2004.
XX
XX 02-DEC-2003; 2003WO-US038234.
XX
XX 02-DEC-2002; 2002US-0430724P.
XX
XX (ABGE-) AGENIX INC.
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
XX Jia X, Nocerini MR;
XX WPI; 2004-461119/43.
XX
XX New human monoclonal antibody that binds to phospholipase A2 (PLA2),
XX useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
XX asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
XX Claim 1; SEQ ID NO 9; 128pp; English.
XX

CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents the heavy chain from a monoclonal antibody
CC that is specific for the human phospholipase A2 (PLA2) enzyme.
XX
XX
SQ Sequence 117 AA;

Query Match 89.9%; Score 558; DB 8; Length 117;
Best Local Similarity 91.4%; Pred. No. 5.1e-44;
Matches 106; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYWGVRQMPGKGLWNGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGSFTYINWVRQMPGKGLWNGIIYPGDSDTRY 60

Qy 61 SPSPQGGVTTISADKSIATYQLQWSSLSKASDTAMYCTR-----GDRGVDYWGQGLTIVTSS 116
Db 61 SPSPQGGVTTISADKSIATYQLQWSSLSKASDTAMYCAHRIGDFDYWGQGLTIVTSS 116

RESULT 9
AAW27555
ID AAW27555 standard; protein; 120 AA.
XX
AC AAW27555;
XX
DT 23-JAN-1998 (first entry)
XX
DE Human Ab heavy chain variable region VH5 consensus.
XX
KW Human; antibody; preparation; library; VH5; variable region; heavy chain;
XX consensus.
XX Homo sapiens.
XX OS
XX WO9708320-A1.
XX
XX PD 06-MAR-1997.
XX
XX PF 19-AUG-1996; 96WO-EP003647.
XX
XX PR 18-AUG-1995; 95EP-00113021.
XX
XX PA (MORP-) MORPHOSYS GBS PROTEINOPTIMIERUNG MBH.
XX
XX PI Knappik A, Pack P, Ilag V, Ge L, Moroney S, Plueckthun A;
XX
XX DR WPI; 1997-179277/16.
XX
XX DR N-ESDB; AAT87953.
XX
XX PT Preparation of human derived antibody gene library - using synthetic
XX consensus sequences, and signal consensus antibody gene as universal
XX framework for highly diverse antibody libraries.
XX
XX PS Example 1; Fig 5F; 436pp; English.
XX
XX CC The present sequence is the human antibody heavy chain variable region
XX synthetic sequence VH5, used in the preparation of a human derived
XX antibody gene library
XX
SQ Sequence 120 AA;

Query Match 89.5%; Score 556; DB 2; Length 120;
Best Local Similarity 89.2%; Pred. No. 8e-44;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYWGVRQMPGKGLWNGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGSFTSYWGVRQMPGKGLWNGIIYPGDSDTRY 60

Qy 61 SPSPQGGVTTISADKSIATYQLQWSSLSKASDTAMYCTR-----GDRGVDYWGQGLTIVTSS 116
Db 61 SPSPQGGVTTISADKSIATYQLQWSSLSKASDTAMYCAHRIGDFDYWGQGLTIVTSS 120

RESULT 10
ABJ18677
ID ABJ18677 standard; protein; 120 AA.
XX
AC ABJ18677;
XX
DT 06-MAR-2003 (first entry)
XX
DE Antibody library related heavy variable chain protein region SEQ ID No 6.
XX
KW Library; recombinant antibody; clustering variable region; in silico;
XX immunogenicity; antibody therapeutic.
XX
XX OS Unidentified.
XX
XX FN WO200284277-A1.
XX
XX PD 24-OCT-2002.
XX
XX PF 17-APR-2002; 2002WO-US012202.
XX
XX PR 17-APR-2001; 2001US-0284407P.
XX
XX PA (ABMA-) ABMAXIS INC.
XX
XX PI Luo P;
XX
XX DR WPI; 2003-093043/08.
XX
XX PT Constructing a library of recombinant antibodies useful as source of
XX antibody candidates for screening antigens comprises clustering variable
XX regions of antibodies having known 3-dimensional structures into
XX structural ensembles.
XX
XX PS Disclosure; Page 102-103; 119pp; English.

The invention relates to a novel method for the construction of a library of recombinant antibodies. The novel method comprises clustering variable regions of a collection of antibodies having known 3D structures into at least two families of structural ensembles, each comprising at least two different antibody sequences but with substantially identical main chain conformations. The method is useful for constructing a library of artificial antibodies in silico which provides a structurally diverse and yet functionally more relevant source of antibody candidates which can then be screened for binding a wide variety of target molecules, including small molecules, and biomacromolecules such as proteins, peptides and nucleic acids. The libraries constructed are useful as a source of antibody candidates for further screening for novel antibodies with high affinity against a wide range of antigens and having no or minimum immunogenicity to human subjects treated with antibody therapeutics. This sequence represents a protein region of an antibody relating to the novel antibody library construction method of the invention

Sequence 120 AA;
Query Match 89.5%; Score 556; DB 6; Length 120;
Best Local Similarity 89.2%; Pred. No. 8e-44;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYWGVRQMPGKGLWNGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGSFTSYWGVRQMPGKGLWNGIIYPGDSDTRY 60

Qy 61 SPSPQGGVTTISADKSIATYQLQWSSLSKASDTAMYCTR-----GDRGVDYWGQGLTIVTSS 116
Db 61 SPSPQGGVTTISADKSIATYQLQWSSLSKASDTAMYCAHRIGDFDYWGQGLTIVTSS 120


```
RESULT 11
ABJ18720
ID ABJ18720 standard; protein, 120 AA.
XX
AC ABJ18720;
XX
DT 06-MAR-2003 (first entry)
XX
DE Antibody library related VH protein region 1DHW.
XX
KW Library; recombinant antibody; clustering variable region; in silico;
KW immunogenicity; antibody therapeutic.
XX
OS Unidentified.
XX
PN WO200284277-A1.
XX
PD 24-OCT-2002.
XX
PF 17-APR-2002; 2002WO-US012202.
XX
PR 17-APR-2001; 2001US-0284407P.
XX
PA (ABMA-) ABMAXIS INC.
XX
PI Luo P;
XX
DR WPI; 2003-093043/08.
XX
PT Constructing a library of recombinant antibodies useful as source of
PT antibody candidates for screening antigens comprises clustering variable
PT regions of antibodies having known 3-dimensional structures into
PT structural ensembles.
XX
PS Disclosure; Fig 13B; 119pp; English.
XX
CC The invention relates to a novel method for the construction of a library
CC of recombinant antibodies. The novel method comprises clustering variable
CC regions of a collection of antibodies having known 3D structures into at
CC least two families of structural ensembles, each comprising at least two
CC different antibody sequences but with substantially identical main chain
CC conformations. The method is useful for constructing a library of
CC artificial antibodies in silico which provides a structurally diverse and
CC yet functionally more relevant source of antibody candidates which can
CC then be screened for binding a wide variety of target molecules,
CC including small molecules, and biomacromolecules such as proteins,
CC peptides and nucleic acids. The libraries constructed are useful as a
CC source of antibody candidates for further screening for novel antibodies
CC with high affinity against a wide range of antigens and having no or
CC minimum immunogenicity to human subjects treated with antibody
CC therapeutics. This sequence represents a protein region of an antibody
CC relating to the novel antibody library construction method of the
CC invention
XX
SQ Sequence 120 AA;
Query Match 89.5%; Score 556; DB 6; Length 120;
Best Local Similarity 89.2%; Pred. No. 8e-44;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
QY 1 EVQLVQSGAEVKKPKQESLRISCKGSGDSFTTWIGVROMPGKLEWNGIIVPGSDTIY 60
DB 1 EVQLVQSGAEVKKPKQESLRISCKGSGDSFTTWIGVROMPGKLEWNGIIVPGSDTRY 60
QY 61 SPSPFGQVTTISADKSIISTAYLOWSSLKASDTAMYCYCTR---GDRGVYWGQGTLLVTVSS 116
DB 61 SPSPFGQVTTISADKSIISTAYLOWSSLKASDTAMYCARWGGDGFYANDYWGQGTLLVTVSS 120
RESULT 12
ABP45526
ID ABP45526 standard; protein, 252 AA.
XX
AC ABP45526;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLYS binding scFv SEQ ID 1537.
XX
KW BLYS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2237-2238; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (BLYS) polypeptides. BLYS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS
CC and so may be used to detect and quantitate the presence of BLYS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLYS. They may also be
CC administered to treat diseases associated with aberrant BLYS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 252 AA;
Query Match 89.0%; Score 552.5; DB 5; Length 252;
Best Local Similarity 84.8%; Pred. No. 3.7e-43;
Matches 106; Conservative 4; Mismatches 6; Indels 9; Gaps 1;
QY 1 EVQLVQSGAEVKKPKQESLRISCKGSGDSFTTWIGVROMPGKLEWNGIIVPGSDTIY 60
DB 1 EVQLVQSGAEVKKPKQESLRISCKGSGDSFTTWIGVROMPGKLEWNGIIVPGSDTRY 60
QY 61 SPSPFGQVTTISADKSIISTAYLOWSSLKASDTAMYCYCTR-----RGVDYWGQGTLL 111
DB 61 SPSPFGQVTTISADKSIISTAYLOWSSLKASDTAMYCARLDYDILGTLYYPSGDFYWGQGT 120
```



```
QY 1 EVLVQSGAEVKKPGESLRISCKGSDSFTTWIGWVRQMPKGLWGMGIIPGSDTIY 60
Db 12 EVLVQSGAEVKKPGESLRISCKGSGYSFTSYIGWVRQMPKGLWGMGIIPGSDTRY 71
QY 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRY-----GDRGVDYWGQGLTVTVS 115
Db 72 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRYAVAGHYFDYWGQGLTVTVS 131
QY 116 S 116
Db 132 S 132

RESULT 15
ADP47229
ID ADP47229 standard; protein; 117 AA.
AC ADP47229;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human phospholipase A2-specific monoclonal antibody heavy chain #27.
XX
KW human; monoclonal antibody; phospholipase A2; PLA2;
KW inflammatory disorder; degenerative disorder;
KW joint inflammatory reaction; skin inflammatory reaction;
KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS Homo sapiens.
XX
PN WO2004050850-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038234.
XX
PR 02-DEC-2002; 2002US-0430724P.
XX
PA (ABGE-) ABGENIX INC.
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
PI Jia X, Nocerini MR;
XX
WPI: 2004-461119/43.
XX
PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS Example 5; SEQ ID NO 144; 128pp; English.
XX
CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents the heavy chain from a monoclonal antibody
CC that is specific for the human phospholipase A2 (PLA2) enzyme.
XX
SQ Sequence 117 AA;

Query Match 88.9%; Score 552; DB 8; Length 117;
Best Local Similarity 89.7%; Pred. NO. 1.8e-43;
Matches 104; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVLVQSGAEVKKPGESLRISCKGSDSFTTWIGWVRQMPKGLWGMGIIPGSDTIY 60
Db 1 EVLVQSGAEVKKPGESLRISCKGSGYSFTSYIGWVRQMPKGLWGMGIIPGSDTRY 60
QY 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTRYGDRGVDYWGQGLTVTVS 116
```

Db 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCARXXXAFDIWGQGTWTVTVSS 116

Search completed: December 3, 2005, 14:25:01
Job time : 200.384 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:48 ; Search time 204.539 Seconds
(without alignments)
400.126 Million cell updates/sec

Title: US-10-769-144-4

Perfect score: 621

Sequence: 1 EVQLVQSGAEVKKPGESLR.....TRGDRGVDMGQGLTVTVSS 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	434	69.9	475	Q5RE17_PONPY	Q5re17 pongo pygma
2	389	62.6	124	Q9UL92_HUMAN	Q9ul92 homo sapien
3	381.5	61.4	119	Q9UL94_HUMAN	Q9ul94 homo sapien
4	379	61.0	118	Q9Z1C4_MOUSE	Q9z1c4 mus musculus
5	379	61.0	590	Q4V9V8_MOUSE	Q4v9v8 mus musculus
6	374.5	60.3	614	Q7TMT6_MOUSE	Q7tmt6 mus musculus
7	372.5	60.0	244	Q65ZC8_HUMAN	Q65zc8 homo sapien
8	372.5	60.0	481	Q91WT1_MOUSE	Q91wt1 mus musculus
9	372	59.9	498	Q6N041_HUMAN	Q6n041 homo sapien
10	369.5	59.5	458	Q5BJZ2_RAT	Q5bjz2 rattus norv
11	367.5	59.2	125	Q9UL95_HUMAN	Q9ul95 homo sapien
12	366.5	59.0	473	Q9D8L4_MOUSE	Q9d8l4 mus musculus
13	362.5	58.4	480	Q6P089_HUMAN	Q6p089 homo sapien
14	359	57.8	116	Q9UL89_HUMAN	Q9ul89 homo sapien
15	358.5	57.7	146	Q924Q3_MOUSE	Q924q3 mus musculus
16	358.5	57.7	616	Q504M7_MOUSE	Q504m7 mus musculus
17	358	57.6	518	Q6N030_HUMAN	Q6n030 homo sapien
18	357.5	57.6	120	HV1F_HUMAN	P63226 homo sapien
19	356.5	57.4	125	Q5F2I1_MOUSE	Q5f2i1 mus musculus
20	356	57.3	143	Q924Q0_MOUSE	Q924q0 mus musculus
21	356	57.3	617	Q4KML5_MOUSE	Q4kml5 mus musculus
22	355	57.2	159	Q96QSO_HUMAN	Q96qso homo sapien
23	355	57.2	482	Q8K172_MOUSE	Q8k172 mus musculus
24	354.5	57.1	119	Q9GYZ2_MOUSE	Q9gyz2 mus musculus
25	354.5	57.1	142	Q924Q1_MOUSE	Q924q1 mus musculus
26	354.5	57.1	464	Q6PF95_MOUSE	Q6pf95 mus musculus
27	354.5	57.1	483	Q5Z153_MOUSE	Q5z151 mus musculus
28	354	57.0	143	Q924R0_MOUSE	Q924r0 mus musculus
29	353.5	56.9	519	Q5EBM2_HUMAN	Q5ebm2 homo sapien
30	353	56.8	141	Q924Q4_MOUSE	Q924q4 mus musculus
31	353	56.8	145	Q924R4_MOUSE	Q924r4 mus musculus

32 352.5 56.8 121 1 HV01_MOUSE P01745 mus musculus
33 352.5 56.8 468 2 Q569W9_MOUSE Q569w9 mus musculus
34 352 56.7 243 2 Q7TQM2_MOUSE Q7tqm2 mus musculus
35 351 56.5 469 2 Q7Z7P5_HUMAN Q7z7p5 homo sapien
36 351 56.5 475 2 Q6N095_HUMAN Q6n095 homo sapien
37 350 56.4 136 2 Q7TPE3_MOUSE Q7tpe3 mus musculus
38 350 56.4 145 2 Q924R1_MOUSE Q924r1 mus musculus
39 349 56.2 143 2 Q924P9_MOUSE Q924p9 mus musculus
40 349 56.2 145 2 Q924P7_MOUSE Q924p7 mus musculus
41 349 56.2 465 2 Q6PJB2_MOUSE Q6pjb2 mus musculus
42 348.5 56.1 474 2 Q8R3H6_MOUSE Q8r3h6 mus musculus
43 348.5 56.1 598 2 Q568Y0_RAT Q568y0 rattus norv
44 348 56.0 463 2 Q99LC4_MOUSE Q99lc4 mus musculus
45 347.5 56.0 140 2 Q924R2_MOUSE Q924r2 mus musculus

ALIGNMENTS

RESULT 1
Q5RE17_PONPY
ID Q5RE17_PONPY PRELIMINARY; PRT; 475 AA.
AC Q5RE17;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp469C2335.
GN Name=DKFZp469C2335;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR857722; CAH89990.1; -, mRNA.
DR SMR; Q5RE17; 21-475.
DR GO; GO:0030106; P:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51998 MW; 04BBD5096A2CD529 CRC64;

Query Match 69.9%; Score 434; DB 2; Length 475;

Best Local Similarity 68.0%; Pred. No. 2.8e-35;

Matches 85; Conservative 13; Mismatches 17; Indels 10; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLRISCKGSDSFTTYWGVMQPMCKGLHWGIIYPGSDITLY 60

DB 20 DIQLVQSGAEVKKPGESLRISCKGSGYFTTYWGVMQPMCKGLHWGIIYPGSDITLY 79

QY 61 SPSPGQVITISADKSIISTAYLQWSLKASDIAWYCTR----GDRG-----VDYWGQGT 110

DB 80 NRSFPGHITISADMSISTAYLQWTSLKASDSAIYICARLRLSGTNSYHKRSYFQFWGQGT 139

QY 111 LVTVS 115

[illegible][illegible]

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AC Q65ZC8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
GN Single-chain Fv (Fragment).
DS Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13057; CAA73500.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00406; IGV; 2.
DR PROSITE; PS00356; IG_v.
DR PROSITE; PS00359; IG LIKE; 2.
FT NON_TER 1
FT NON_TER 244
FT NON_TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17869338F2BF CRC64;

Query Match 60.0%; Score 372.5; DB 2; Length 244;
Best Local Similarity 57.9%; Pred. No. 2.2e-29;
Matches 70; Conservative 23; Mismatches 23; Indels 5; Gaps 1;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGDSFTYYIGWVRQMPGKGLNWGIYPGDSSTIY 60
Db 1 QVQLVQSGAEVKPGDSVKVSKASGYTFSDFYHMHVRAQPGQGLNWGMDPNNGDTRF 60

Qy 61 SPSPGQGVTTISADKSIATYQLWSSLSKASDTAMYCTRGDR-----GVDYWGQGLTVTVS 115
Db 61 AQRFGQVTRDTRTSIAAYMEVSRSLSDDTAVYICAREGTGSAIYGMVDWVGQGLTVTVS 120

Qy 116 S 116
Db 121 S 121

RESULT 8
Q91WT1_MOUSE
ID Q91WT1_MOUSE PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=2238255; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., USCIN T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -; mRNA.
DR HSP; P01751; 1A6W.
DR EMBL; ENSMUSG000000021155; Mus musculus.
GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 60.0%; Score 372.5; DB 2; Length 481;
Best Local Similarity 59.0%; Pred. No. 4.6e-29;
Matches 69; Conservative 23; Mismatches 24; Indels 1; Gaps 1;

Qy 1 EVQLVQSGAEVKPGESLRISCKGSGDSFTYYIGWVRQMPGKGLNWGIYPGDSSTIY 60
Db 20 QVQLVQSGPELVPGASVKISKASGYTFTSYTHVVKRPGQGLVIGWYPGDGNTKY 79

Qy 61 SPSPGQGVTTISADKSIATYQLWSSLSKASDTAMYCTRGDR-GVDYWGQGLTVTVS 116
Db 80 NEKFKGKTKTLTADKSSSTAYMFLSLTSDSAVYFCTRGGGAFFYWGQGLTVTVS 136

RESULT 9
Q6N041_HUMAN
ID Q6N041_HUMAN PRELIMINARY; PRT; 498 AA.
AC Q6N041;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686O16217 (Fragment).
GN Name=DKFZp686O16217;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Human rectum tumor;
RX The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640710; CAA54829.1; -; mRNA.
DR HSP; P01751; 1A6W.
DR SMR; Q6N041; 268-476.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 4.
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DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;

Query Match          59.9%; Score 372; DB 2; Length 498;
Best Local Similarity 56.5%; Pred. No. 5.4e-29;
Matches 70; Conservative 20; Mismatches 26; Indels 8; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYIGWVQMPKGLGIEWMGIYVPGSDTIY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 35 QVQLVQSGADVKKPKGASVKVSKASGYTFITNYFFHWVRQAPQGQPEWGMINPRDGS TKY 94

QY 61 SPFGQGVTTISADKSIISTAYLQWSLSKASDTAMYYCTRGD-----VDYWGQGTILV 112
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 95 AQRFQGRVSMTRDTSITAYMELSLRSRSDTAMFFCARAGPGYGTSAYSYFYDYGQGTILV 154

QY 113 TVSS 116
DB 155 TVSS 158

RESULT 10
Q5BJ22 RAT PRELIMINARY; PRT; 458 AA.
AC Q5BJ22;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE LOC367586 protein.
GN Name=LOC367586;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins E.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC091272; AAH91272.1; -; mRNA.
DR SMR; Q5BJ22; 21-454.

DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;

Query Match          59.5%; Score 369.5; DB 2; Length 458;
Best Local Similarity 59.0%; Pred. No. 8.8e-29;
Matches 69; Conservative 20; Mismatches 27; Indels 1; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYIGWVQMPKGLGIEWMGIYVPGSDTIY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 20 QVQLVQSGAEVKKPGSSVKISCKASGYTFITNYDTHWKIQQPGNGLEWIGIYFGNGTKY 79

QY 61 SPFGQGVTTISADKSIISTAYLQWSLSKASDTAMYYCTRG-DRGVVDYWGQGTILVTVSS 116
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 80 NQKNGKATLTADKSSSTAYWQLSLTSDSADVFCARDYDFGVDYWGQGVMTVTVSS 136

RESULT 11
Q5UL95 HUMAN PRELIMINARY; PRT; 125 AA.
AC Q5UL95;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035019; AAD56255.1; -; mRNA.
DR HSSP; P01751; INQB.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER
FT NON TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match          59.2%; Score 367.5; DB 2; Length 125;
Best Local Similarity 56.0%; Pred. No. 3.4e-29;
Matches 70; Conservative 19; Mismatches 27; Indels 9; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYIGWVQMPKGLGIEWMGIYVPGSDTIY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 EVQLVESGAELVKPGASVKVSKASGYTFITGYIMHWVRQAPQGQGLEWGMINPSGNTY 60

QY 61 SPFGQGVTTISADKSIISTAYLQWSLSKASDTAMYYCTRGD-----VDYWGQGTIL 111
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 AQKVGQVMTVTDITISTAYMELSLRSDDTAVVYCARSGQGGRIAAAGDAFDWQGTIM 120

QY 112 VTSS 116
DB 121 VTSS 125
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RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwaige K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.",
Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK007918; BAB25349.1; -, mRNA.
DR PIR; PH1165; PH1165.
DR PIR; S26746; S26746.
DR HSP; P01864; IBOG.
DR SMR; Q9D8L4; 20-469.
DR ENSEMBL; ENSMUSG0000054328; Mus musculus.
DR MGI; MGI:96443; Igh-1a.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0005771; C:multivesicular body; IDA.
DR GO; GO:0003823; P:antigen binding; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0003033; P:antigen processing; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0008333; P:endosome to lysosome transport; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0050871; P:positive regulation of B cell activation; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type II hypersensitivity; IDA.
DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
Query Match 59.0%; Score 366.5; DB 2; Length 473;
Best Local Similarity 58.0%; Pred. No. 1.8e-28;
Matches 69; Conservative 20; Mismatches 27; Indels 3; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGSFYYTWMVGMVQPKGLEWGLIYPGDSSTIY 60
Db 20 QVQLKQSGAEVKKPGASVKGVTFDYINWVQKRPQGLKIGKIPGSGSTYY 79
Qy 61 SPSPQGVTTISADKSIATYLOWSSLSKASDTAMVYCTRGDRGVDP---YWGQGLTVTVSS 116
Db 80 NEKFKGKATITADSSSTAYWQLSLSSESAVFCARSGVDYDWFAYWGQGLTVTVSA 138
RESULT 13
Q6P089_HUMAN
ID Q6P089_HUMAN PRELIMINARY; PRT; 480 AA.

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwaige K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.",
Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK007918; BAB25349.1; -, mRNA.
DR PIR; PH1165; PH1165.
DR PIR; S26746; S26746.
DR HSP; P01864; IBOG.
DR SMR; Q9D8L4; 20-469.
DR ENSEMBL; ENSMUSG0000054328; Mus musculus.
DR MGI; MGI:96443; Igh-1a.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0005771; C:multivesicular body; IDA.
DR GO; GO:0003823; P:antigen binding; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0003033; P:antigen processing; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0008333; P:endosome to lysosome transport; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0050871; P:positive regulation of B cell activation; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type II hypersensitivity; IDA.
DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
Query Match 59.0%; Score 366.5; DB 2; Length 473;
Best Local Similarity 58.0%; Pred. No. 1.8e-28;
Matches 69; Conservative 20; Mismatches 27; Indels 3; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGSFYYTWMVGMVQPKGLEWGLIYPGDSSTIY 60
Db 20 QVQLKQSGAEVKKPGASVKGVTFDYINWVQKRPQGLKIGKIPGSGSTYY 79
Qy 61 SPSPQGVTTISADKSIATYLOWSSLSKASDTAMVYCTRGDRGVDP---YWGQGLTVTVSS 116
Db 80 NEKFKGKATITADSSSTAYWQLSLSSESAVFCARSGVDYDWFAYWGQGLTVTVSA 138
RESULT 13
Q6P089_HUMAN
ID Q6P089_HUMAN PRELIMINARY; PRT; 480 AA.

```
AC Q6P089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RC NUCLEOTIDE SEQUENCE.
TX TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan E., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
TX TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065733; AAH5733.1; -, mRNA.
DR HSSP; P01751; IAGW.
DR SMR; Q6P089; 250-458.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 51997 MW; 2E286C57E4F0ED65 CRC64;

Query Match 58.4%; Score 362.5; DB 2; Length 480;
Best Local Similarity 57.9%; Pred. No. 4.7e-28;
Matches 70; Conservative 19; Mismatches 27; Indels 5; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYWGVRQMPGKGLVWMGIYPGSDTIY 60
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLVQSGAEVKKTKASVKVSKASGYISDNIHVVQAPQGLVWAWIRPQNGITVS 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCYTRGDRG-----VDYWGQGLTVTVS 115
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AEKFGQVRVTTITDTSINTAYMELTSLKSDDTALYICARGHSDWSSYFYDYGQGLTVTVS 139
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 116 $ 116
Db 140 $ 140
```

```
RESULT 14
Q9UL89 HUMAN PRELIMINARY; PRT; 116 AA.
AC Q9UL89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RC NUCLEOTIDE SEQUENCE.
TX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4533;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
TX PubMed=1660528;
RA Manheimer-Lofy A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype.";
RL J. Exp. Med. 174:1639-1652 (1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
TX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA Hillson J.L., Karr N.S., Opplinger I.R., Mannik M., Sasso E.H.;
RT "The structural basis of germline-encoded VH3 immunoglobulin binding
RT to staphylococcal protein A.";
RL J. Exp. Med. 178:331-336 (1993).
DR EMBL; AF035025; AAD56261.1; -, mRNA.
DR PIR; PH0870; PH0870.
DR PIR; PH1671; PH1671.
DR HSSP; P01751; INQB.
DR SMR; Q9UL89; 1-115.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match 57.8%; Score 359; DB 2; Length 116;
Best Local Similarity 60.3%; Pred. No. 2.3e-28;
Matches 70; Conservative 17; Mismatches 25; Indels 4; Gaps 1;

QY 5 VQSGAEVKKPGESLRISCKGSGDFTTYWGVRQMPGKGLVWMGIYPGSDTIYSPSF 64
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 VQSGAEVKKPGSSVKVSKASGTFSSVAISWVRQAPQGLVWGRIRIIPILGIANYAKF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 65 QGQVTTISADKSIISTAYLQWSSLKASDTAMYCYTRGDRG-----VDYWGQGLTVTVS 116
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 QGRVTTITADKSTAYMELSLRSEDYAVYYCASSNNGPYWYFDLWGRGTLTVTVSS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 15
Q924Q3 MOUSE PRELIMINARY; PRT; 146 AA.
AC Q924Q3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:11:59 ; Search time 31.7224 Seconds
(without alignments)
351.837 Million cell updates/sec

Title: US-10-769-144-4
Perfect score: 621
Sequence: 1 EVQLVQSGAEVKPGESLR1.....TRGDRGVDMGQGLTVTVSS 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	548	88.2	139	PH1558	Ig heavy chain V r
2	543.5	87.5	113	PH1428	Ig heavy chain V r
3	541.5	87.2	127	PH1414	Ig heavy chain V r
4	540.5	87.0	136	PH1559	Ig heavy chain V r
5	536.5	86.4	123	C36006	Ig heavy chain V r
6	535	86.2	136	A49047	Ig heavy chain V r
7	534.5	86.1	123	S38492	Ig heavy chain - h
8	529.5	85.3	127	PH1415	Ig heavy chain V r
9	525.5	84.6	123	PH1413	Ig heavy chain V r
10	525.5	84.6	127	PH1411	Ig heavy chain V r
11	524.5	84.5	123	PH1423	Ig heavy chain V r
12	520	83.7	134	PH1422	Ig heavy chain V r
13	519.5	83.7	117	S19670	Ig heavy chain V r
14	519.5	83.7	127	PH1420	Ig heavy chain V r
15	513.5	82.7	117	S19669	Ig heavy chain V r
16	510	82.1	137	PH1562	Ig heavy chain V r
17	508	81.8	126	PH1424	Ig heavy chain V r
18	508	81.8	126	PH1419	Ig heavy chain V r
19	505	81.3	126	PH1416	Ig heavy chain V r
20	504.5	81.2	138	PH1565	Ig heavy chain V r
21	502	80.8	126	PH1417	Ig heavy chain V r
22	502	80.8	126	PH1418	Ig heavy chain V r
23	500	80.5	126	PH1412	Ig heavy chain V r
24	499.5	80.4	125	PH1410	Ig heavy chain V r
25	496.5	80.0	138	PH1564	Ig heavy chain V r
26	496	79.9	122	PH1426	Ig heavy chain V r
27	495	79.7	98	S26907	Ig heavy chain V r
28	495	79.7	101	S12424	Ig heavy chain V r
29	495	79.7	102	PH1279	Ig heavy chain V r

ALIGNMENTS

RESULT 1

PH1558
Ig heavy chain V region (clone DOB) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 16-Aug-1996
C:Accession: PH1558
R:Rassenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A:Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymphocytic leukemia
A:Reference number: PH1557; MUID:93210459; PMID:7681468
A:Accession: PH1558
A:Molecule type: DNA
A:Residues: 1-139 <RAS>

A:Cross-references: UNIPARC:UPI0000176581
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <IMV>

Query Match 88.2%; Score 548; DB 2; Length 139;
Best Local Similarity 86.9%; Pred. No. 1.9e-44;
Matches 106; Conservative 2; Mismatches 8; Indels 6; Gaps 1;

Oy	1	EVQLVQSGAEVKPGESLRISCKGSGDSFTTYWIGWVRQMPGKGLWMGIIYPGSDTRIY	60
Db	18	EVQLVQSGAEVKPGESLRISCKGSGYSFTSYWIGWVRQMPGKGLWMGIIYPGSDTRY	77
Oy	61	SPSFGQVTISADKSIISTAYLQWSSLKASDTAMYYCTRG-----DRGVDYWGQGLTVTV	114
Db	78	SPSFGQVTISADKSIISTAYLQWSSLKASDTAMYYCARSISSSGYSNFDYWGQGLTVTV	137
Oy	115	SS 116	
Db	138	SS 139	

RESULT 2

PH1428
Ig heavy chain V region (clone VH5-1R1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 28-May-1999
C:Accession: PH1428
R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of somatic mutations
A:Reference number: PH1409; MUID:93115676; PMID:8418213
A:Accession: PH1428
A:Molecule type: mRNA
A:Residues: 1-113 <VAN>
A:Cross-references: UNIPARC:UPI0000176877; GB:S51905; NID:9262690; PIDN:AAC80261.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 543.5; DB 2; Length 113;
Best Local Similarity 89.7%; Pred. No. 4e-44;
Matches 104; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSDTIY 60
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDGVYWGQGLTIVTSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYYCA---RAFDVWGQGLTIVTSS 113

RESULT 3

Ig heavy chain V region (clone P1-54) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C/Accession: PH1414
J. Exp. Med. 177, 99-107, 1993
A/Title: Molecular evolution of the human immunoglobulin E response: High incidence of somatic hypermutation
A/Reference number: PH1409; MUID:931115676; PMID:8418213
A/Accession: PH1414
A/Molecule type: mRNA
A/Residues: 1-127 <VAN>
A/Cross-references: UNIPARC:UPI000017694E
A/Experimental source: PMBC
A/Note: the authors translated the codon TTG for residue 119 as Met
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 541.5; DB 2; Length 127;
Best Local Similarity 85.4%; Pred. No. 7e-44;
Matches 105; Conservative 3; Mismatches 8; Indels 7; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSDTIY 60
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGD-----RGVDYWGQGLTIVT 113
Db 61 SPSPGQGVTTISADKSIISTAYLQWSSLKATDTAMYYCARRDYQSTGGDFPVGQGLTIVT 120
Qy 114 VSS 116
Db 121 VSS 123

RESULT 4

Ig heavy chain V region (clone HAN) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
C/Accession: PH1559
R. Sessenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A/Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymphocytic leukemia
A/Reference number: PH1557; MUID:93210459; PMID:7681468
A/Accession: PH1559
A/Molecule type: DNA
A/Residues: 1-136 <RAS>
A/Cross-references: UNIPARC:UPI0000176A21
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 540.5; DB 2; Length 136;
Best Local Similarity 89.1%; Pred. No. 9.3e-44;

Matches 106; Conservative 2; Mismatches 8; Indels 3; Gaps 2;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSDTIY 60
Db 18 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSDTIY 77
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYYCTR--GD-RGVDYWGQGLTIVTSS 116
Db 78 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYYCARLYGDFSTVDYWGQGLTIVTSS 136

RESULT 5

Ig heavy chain V region (83p2) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C/Accession: C36006
R. Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene segments in the human immunoglobulin V region
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: C36006
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-123 <SCH>
A/Cross-references: UNIPARC:UPI0000176C49; GB:M34022

C/Genetics:
A/Gene: GDB:IGH@; IGHDI1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 536.5; DB 2; Length 123;
Best Local Similarity 84.6%; Pred. No. 2e-43;
Matches 104; Conservative 4; Mismatches 8; Indels 7; Gaps 1;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTYWIGVWRQMPGKGLWNGIYPGDSDTIY 60
Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDGV-----DYWGQGLTIVT 113
Db 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYYCARHNSQTGASLWYFDLMGRLTIVT 120
Qy 114 VSS 116
Db 121 VSS 123

RESULT 6

Ig heavy chain V region (monoclonal striational autoantibody StrAB SA-1A VH) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C/Accession: A49047
R. Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A/Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A/Reference number: A49047; MUID:92387224; PMID:1516616
A/Accession: A49047
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-136 <VIC>
A/Cross-references: UNIPARC:UPI0000176C6A

A/Experimental source: thymic B lymphocytes
A/Note: sequence extracted from NCBI backbone (NCBIN:113206, NCBI:P:113207)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 535; DB 2; Length 136;
Best Local Similarity 78.8%; Pred. No. 3.1e-43;

```
Matches 104; Conservative 4; Mismatches 8; Indels 16; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFPTTWIGWVRQMPGKGLWVGIIYPGDSDTIY 60
Db 5 EVQLVQSGAEVKKPGESLRISCKGSGDSFPTTWIGWVRQMPGKGLWVGIIYPGDSDTIY 64
Qy 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRTGD-----RGVD 104
Db 65 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRTGD-----RGVD 124
Qy 105 YWGQGLTVVSS 116
Db 125 YWGQGLTVVSS 136

RESULT 7
PHI415
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
R:Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a
A:Reference number: S38492
A:Status: preliminary
A:Accession: S38492
A:Molecule type: DNA
A:Residues: 1-123 <VAR>
A:CROSS-references: UNIPARC:UPI000011654D; EMBL:223034; NID:g414031; PIDN:CAA80569.1; PI
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.1%; Score 534.5; DB 2; Length 123;
Best Local Similarity 84.6%; Pred. No. 3.1e-43;
Matches 104; Conservative 4; Mismatches 8; Indels 7; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFPTTWIGWVRQMPGKGLWVGIIYPGDSDTIY 60
Db 1 QVQLVQSGAEVKKPGESLRISCKGSGDSFPTTWIGWVRQMPGKGLWVGIIYPGDSDTIY 60
Qy 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRTGD-----GDRVDYWGQGLTV 113
Db 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRTGD-----GDRVDYWGQGLTV 120
Qy 114 VSS 116
Db 121 VSS 123

RESULT 8
PHI415
Ig heavy chain V region (clone PI-57) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of
dermatitis.
A:Reference number: PHI409; MUID:93115676; PMID:8418213
A:Accession: PHI415
A:Molecule type: mRNA
A:Residues: 1-127 <VAR>
A:CROSS-references: UNIPARC:UPI000017694F
A:Experimental source: PBMC
A:Note: the authors translated the codon TTG for residue 118 as Met
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 529.5; DB 2; Length 127;
Best Local Similarity 82.1%; Pred. No. 2.2e-42;
Matches 101; Conservative 6; Mismatches 9; Indels 7; Gaps 1;
```

```
Best Local Similarity 84.6%; Pred. No. 9.3e-43;
Matches 104; Conservative 2; Mismatches 10; Indels 7; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFPTTWIGWVRQMPGKGLWVGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFPTTWIGWVRQMPGKGLWVGIIYPGDSDTIY 60
Qy 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRTGD-----RGVDYWGQGLTV 113
Db 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRTGD-----RGVDYWGQGLTV 120
Qy 114 VSS 116
Db 121 VSS 123

RESULT 9
PHI413
Ig heavy chain V region (clone PI-56) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of
dermatitis.
A:Reference number: PHI409; MUID:93115676; PMID:8418213
A:Accession: PHI413
A:Molecule type: mRNA
A:Residues: 1-123 <VAR>
A:CROSS-references: UNIPARC:UPI0000176A34
A:Experimental source: PBMC
A:Note: the authors translated the codon CTG for residue 115 as Met
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.6%; Score 525.5; DB 2; Length 123;
Best Local Similarity 84.0%; Pred. No. 2.1e-42;
Matches 100; Conservative 6; Mismatches 10; Indels 3; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFPTTWIGWVRQMPGKGLWVGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFPTTWIGWVRQMPGKGLWVGIIYPGDSDTIY 60
Qy 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRTGD-----VDYWGQGLTVSS 116
Db 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRTGD-----VDYWGQGLTVSS 119

RESULT 10
PHI411
Ig heavy chain V region (clone PI-53) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of
dermatitis.
A:Reference number: PHI409; MUID:93115676; PMID:8418213
A:Accession: PHI411
A:Molecule type: mRNA
A:Residues: 1-127 <VAR>
A:CROSS-references: UNIPARC:UPI0000176A32
A:Experimental source: PBMC
A:Note: the authors translated the codon TTG for residue 118 as Met
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.6%; Score 525.5; DB 2; Length 127;
Best Local Similarity 82.1%; Pred. No. 2.2e-42;
Matches 101; Conservative 6; Mismatches 9; Indels 7; Gaps 1;
```


Matches 101; Conservative 6; Mismatches 9; Indels 7; Gaps 2;
Qy 1 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYWGVRQMPKGLGWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYWGVRQMPKGLGWNGIIPGDSDTIY 60
Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGV-----DYWGQGLTIVT 113
Db 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGV-----DYWGQGLTIVT 120
Qy 114 VSS 116
Db 121 VPS 123
RESULT 15
S19669
Ig heavy chain V region (VH5DJ) - human
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19669
R:Mark, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
A:Reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19669
A:Molecule type: mRNA
A:Residues: 1-117 <MAR>
A:Cross-references: UNIPARC:UPI0000115FEA; EMBL:X61651; NID:g37731; PIDN:CAA43832.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
Query Match 82.7%; Score 513.5; DB 2; Length 117;
Best Local Similarity 83.8%; Fred. NO. 2.7e-41;
Matches 98; Conservative 7; Mismatches 11; Indels 1; Gaps 1;
Qy 1 EVQLVQSGAEVKPGESLRISCKGSGDSFTTYWGVRQMPKGLGWNGIIPGDSDTIY 60
Db 1 QVQLVQSGAEVKPGESLRISCKGAGYSFTTYWGVRQMPKGLGWNGIIPDSDTRY 60
Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGV-DYWGQGLTIVTSS 116
Db 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGV-DYWGQGLTIVTSS 117

Search completed: December 3, 2005, 14:33:32
Job time : 32.7225 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 13:27:13 ; Search time 159.086 Seconds
(without alignment)
304.667 Million cell updates/sec

Title: US-10-769-144-4

Perfect score: 621

Sequence: 1 EVQLVQSGAEVKKPGESLR.....TRGDRGVDYMGQGLTVTVSS 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA Main:

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	621	100.0	116	3	US-09-851-614-4	Sequence 4, Appli
2	621	100.0	116	4	US-10-035-637-4	Sequence 4, Appli
3	621	100.0	116	5	US-10-769-144-4	Sequence 4, Appli
4	621	100.0	116	5	US-10-903-191-4	Sequence 4, Appli
5	621	100.0	411	5	US-10-769-144-12	Sequence 12, Appli
6	621	100.0	411	5	US-10-903-191-12	Sequence 12, Appli
7	621	100.0	468	5	US-10-769-144-2	Sequence 2, Appli
8	621	100.0	468	5	US-10-903-191-2	Sequence 2, Appli
9	621	100.0	613	5	US-10-769-144-10	Sequence 10, Appli
10	621	100.0	613	5	US-10-903-191-10	Sequence 10, Appli
11	560	90.2	117	5	US-10-726-332-138	Sequence 138, App
12	558	89.9	117	5	US-10-726-332-9	Sequence 9, Appli
13	556	89.5	120	4	US-10-125-687-6	Sequence 6, Appli
14	556	89.5	120	5	US-10-996-191-6	Sequence 6, Appli
15	552.5	89.0	252	3	US-09-880-748-1537	Sequence 1537, Ap
16	552.5	89.0	252	4	US-10-293-418-1337	Sequence 1337, Ap
17	552	88.9	117	5	US-10-726-332-144	Sequence 144, App
18	550.5	88.6	118	5	US-10-726-332-145	Sequence 145, App
19	550	88.6	224	4	US-10-128-520-167	Sequence 167, App
20	550	88.6	224	4	US-10-128-520-170	Sequence 170, App
21	550	88.6	226	4	US-10-128-520-159	Sequence 159, App
22	548.5	88.3	118	5	US-10-726-332-31	Sequence 31, Appli
23	548.5	88.3	118	5	US-10-726-332-134	Sequence 134, App
24	548.5	88.3	138	4	US-10-395-894-27	Sequence 27, Appli
25	548.5	88.3	138	4	US-10-695-667-27	Sequence 27, Appli
26	548.5	88.3	138	5	US-10-976-352-27	Sequence 27, Appli
27	548	88.2	224	4	US-10-128-520-165	Sequence 165, App

28	547	88.1	224	4	US-10-128-520-182	Sequence 182, App
29	546.5	88.0	118	5	US-10-726-332-7	Sequence 7, Appli
30	546.5	88.0	118	5	US-10-726-332-13	Sequence 13, Appli
31	546.5	88.0	118	5	US-10-726-332-29	Sequence 29, Appli
32	546.5	88.0	118	5	US-10-726-332-139	Sequence 139, App
33	545.5	87.8	118	5	US-10-726-332-143	Sequence 143, App
34	545	87.8	116	5	US-10-727-155-166	Sequence 166, App
35	544	87.6	116	5	US-10-727-155-100	Sequence 100, App
36	544	87.6	126	4	US-10-041-860-313	Sequence 313, App
37	544	87.6	224	4	US-10-128-520-164	Sequence 164, App
38	543.5	87.5	118	5	US-10-726-332-15	Sequence 15, Appli
39	543.5	87.5	118	5	US-10-726-332-135	Sequence 135, App
40	543.5	87.5	118	5	US-10-726-332-140	Sequence 140, App
41	543	87.4	224	4	US-10-128-520-180	Sequence 180, App
42	542.5	87.4	118	5	US-10-726-332-141	Sequence 141, App
43	542	87.3	226	4	US-10-128-520-179	Sequence 179, App
44	540.5	87.0	118	5	US-10-726-332-30	Sequence 30, Appli
45	540.5	87.0	225	4	US-10-128-520-162	Sequence 162, App

ALIGNMENTS

RESULT 1
US-09-851-614-4
; Sequence 4, Application US/09851614
; Publication No. US20030167502A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; FILE REFERENCE: MXI-166
; CURRENT APPLICATION NUMBER: US/09/851,614
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USSN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USSN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-614-4
Query Match 100.0%; Score 621; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 8.2e-49;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGSFSTTYWGIVQMPKGLKLEWGGIYPGSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGSFSTTYWGIVQMPKGLKLEWGGIYPGSDTIY 60
Qy 61 SPSPFGQVTTISADKSISTAYLQWSLKASDTAMTYCTRGDRGVDYWGQGLTVTVSS 116
Db 61 SPSPFGQVTTISADKSISTAYLQWSLKASDTAMTYCTRGDRGVDYWGQGLTVTVSS 116
RESULT 2
US-10-035-637-4
; Sequence 4, Application US/10035637
; Publication No. US20030031667A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035,637
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/851,614

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; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US9N 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: US9N 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-035-637-4

Query Match      100.0%; Score 621; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 8.2e-49;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60

Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYICTRGDRGVYWGQGLTLVTSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYICTRGDRGVYWGQGLTLVTSS 116

RESULT 3
US-10-769-144-4
; Sequence 4, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-4

Query Match      100.0%; Score 621; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 8.2e-49;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60

Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYICTRGDRGVYWGQGLTLVTSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYICTRGDRGVYWGQGLTLVTSS 116

RESULT 4
US-10-903-191-4
; Sequence 4, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
```

```
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-4

Query Match      100.0%; Score 621; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 8.2e-49;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60

Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYICTRGDRGVYWGQGLTLVTSS 116
Db 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYICTRGDRGVYWGQGLTLVTSS 116

RESULT 5
US-10-769-144-12
; Sequence 12, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-12

Query Match      100.0%; Score 621; DB 5; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.9e-48;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 142 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIWIGVWRQMPGKGLWNGIIPGDSDTIY 201

Qy 61 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYICTRGDRGVYWGQGLTLVTSS 116
Db 202 SPSPGQGVTTISADKSIISTAYLQWSSLKASDTAMYICTRGDRGVYWGQGLTLVTSS 257

RESULT 6
US-10-903-191-12
; Sequence 12, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
```

; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-12

Query Match 100.0%; Score 621; DB 5; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.9e-48;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVQSGAEVKKPESLRISCKGDSFTTYWIGVQRMPGKGLWNGIIPGSDTIY 60
Db 142 EVQLVQSGAEVKKPESLRISCKGDSFTTYWIGVQRMPGKGLWNGIIPGSDTIY 201
Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGVYWGQGLTVTVSS 116
Db 202 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGVYWGQGLTVTVSS 257

RESULT 7

US-10-769-144-2
; Sequence 2, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-2

Query Match 100.0%; Score 621; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.3e-48;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVQSGAEVKKPESLRISCKGDSFTTYWIGVQRMPGKGLWNGIIPGSDTIY 60
Db 20 EVQLVQSGAEVKKPESLRISCKGDSFTTYWIGVQRMPGKGLWNGIIPGSDTIY 79
Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGVYWGQGLTVTVSS 116
Db 80 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGVYWGQGLTVTVSS 135

RESULT 8

US-10-903-191-2
; Sequence 2, Application US/10903191
; Publication No. US20050180983A1

; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT APPLICATION NUMBER: US/10/903,191
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-2

Query Match 100.0%; Score 621; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.3e-48;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVQSGAEVKKPESLRISCKGDSFTTYWIGVQRMPGKGLWNGIIPGSDTIY 60
Db 20 EVQLVQSGAEVKKPESLRISCKGDSFTTYWIGVQRMPGKGLWNGIIPGSDTIY 79
Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGVYWGQGLTVTVSS 116
Db 80 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGVYWGQGLTVTVSS 135

RESULT 9

US-10-769-144-10
; Sequence 10, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-10

Query Match 100.0%; Score 621; DB 5; Length 613;
Best Local Similarity 100.0%; Pred. No. 4.2e-48;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVQSGAEVKKPESLRISCKGDSFTTYWIGVQRMPGKGLWNGIIPGSDTIY 60
Db 20 EVQLVQSGAEVKKPESLRISCKGDSFTTYWIGVQRMPGKGLWNGIIPGSDTIY 79
Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGVYWGQGLTVTVSS 116
Db 80 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYYCTRGDRGVYWGQGLTVTVSS 135

RESULT 10

US-10-903-191-10
; Sequence 10, Application US/10903191
; Publication No. US20050180983A1
; GENERAL INFORMATION:
; APPLICANT: Keller, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Rana Krishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MXI-301CP
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US/10/903,191
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/769144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-903-191-10

Query Match 100.0%; Score 621; DB 5; Length 613;
Best Local Similarity 100.0%; Pred. No. 4.2e-48;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYTWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 20 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYTWIGVWRQMPGKGLWNGIIPGDSDTIY 79
Qy 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116
Db 80 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 135

RESULT 11
US-10-726-332-138
; Sequence 138, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: 99, 100, 102
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-726-332-138

Query Match 90.2%; Score 560; DB 5; Length 117;
Best Local Similarity 91.4%; Pred. No. 2.9e-43;
Matches 106; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYTWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYTWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Qy 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116
Db 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116

RESULT 12
US-10-726-332-9
; Sequence 9, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-9

Query Match 89.9%; Score 558; DB 5; Length 117;
Best Local Similarity 91.4%; Pred. No. 4.4e-43;
Matches 106; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYTWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDFTTYTWIGVWRQMPGKGLWNGIIPGDSDTIY 60
Qy 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116
Db 61 SPSPGQQTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGVYWGQGLTVTVSS 116

RESULT 13
US-10-125-687-6
; Sequence 6, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/125,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-125-687-6

Query Match 89.5%; Score 556; DB 4; Length 120;
Best Local Similarity 89.2%; Pred. No. 6.9e-43;

Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPKGLKLEWMGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPKGLKLEWMGIIYPGDSDTIY 60
Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTTR-----GDRGVYWGQGLTLVTSS 116
Db 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTTR-----GDRGVYWGQGLTLVTSS 120

RESULT 14

US-10-996-191-6
; Sequence 6, Application US/10996191
; Publication No. US20050148001A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705.301
; CURRENT APPLICATION NUMBER: US/10/996,191
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-996-191-6

Query Match 89.5%; Score 556; DB 5; Length 120;
Best Local Similarity 89.2%; Pred. No. 6.9e-43;
Matches 107; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPKGLKLEWMGIIYPGDSDTIY 60
Db 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPKGLKLEWMGIIYPGDSDTIY 60
Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTTR-----GDRGVYWGQGLTLVTSS 116
Db 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTTR-----GDRGVYWGQGLTLVTSS 120

RESULT 15

US-09-880-748-1537
; Sequence 1537, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1537
; LENGTH: 252
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-880-748-1537

Query Match 89.0%; Score 552.5; DB 3; Length 252;
Best Local Similarity 84.8%; Pred. No. 3e-42;
Matches 106; Conservative 4; Mismatches 9; Indels 9; Gaps 1;
Qy 1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPKGLKLEWMGIIYPGDSDTIY 60
Db 1 QVQLVQSGAEVKKPGESLRISCKGSGDSFTTWIGWVRQMPKGLKLEWMGIIYPGDSDTIY 60

Qy 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTTR-----RGVDYWGQGLTL 111
Db 61 SPSPGQVTTISADKSIISTAYLQWSSLKASDTAMYCTTR-----RGVDYWGQGLTL 120
Qy 112 VTVSS 116
Db 121 VTVSS 125

Search completed: December 3, 2005, 14:17:33
Job time : 160.086 secs

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Db      61 SPSPQGVTTISADKSIISTAYLQWSSLKASDTAMYICARLDYDILTGYVPSGFDYWGQGT 120
Qy      112 VTSS 116
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Db      121 VTSS 125

RESULT 2
US-11-054-515-1312
; Sequence 1312, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1312
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1312

Query Match      84.5%; Score 524.5; DB 7; Length 249;
Best Local Similarity 81.6%; Pred. No. 5.6e-47;
Matches 102; Conservative 5; Mismatches 9; Indels 9; Gaps 1;

Qy      1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIGWVRQMPGKGLWNGIIYPGDSDTIY 60
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 QVQLVQSGAEVKKPGESLRISCKGSGYSFTYIWGWVRQMPGKGLWNGIIPGDSNTRY 60
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      61 SPSPQGVTTISADKSIISTAYLQWSSLKASDTAMYICRGRGV-----DYWGQGT 111
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 SPSPQGVTTISADKSIISTAYLQWSSLKASDTAMYICARLYDYDILTGYHDAFDIWGQGT 120
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      112 VTSS 116
        |||||
Db      121 VTSS 125

RESULT 3
US-11-054-515-2088
; Sequence 2088, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1312
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1312

Query Match      80.7%; Score 501; DB 7; Length 248;
Best Local Similarity 81.1%; Pred. No. 1.4e-44;
Matches 99; Conservative 4; Mismatches 13; Indels 6; Gaps 1;

Qy      1 EVQLVQSGAEVKKPGESLRISCKGSGDSFTYYIGWVRQMPGKGLWNGIIPGDSDTIY 60
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVQLVQSGAEVKKPGESLRISCKGSGYSFTSYIWGWVRQMPGKGLWNGRIDPSDSYTN 60
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      61 SPSPQGVTTISADKSIISTAYLQWSSLKASDTAMYICTR-----GDRGVDTYWGQGT 114
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 SPSPQGVTTISADKSIISTAYLQWSSLKASDTAIYICARRGTSNYSYSGMDVWGQGT 120
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      115 SS 116
        ||
Db      121 SS 122

RESULT 4
US-11-054-515-1
; Sequence 1, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
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; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1

Query Match      80.2%; Score 498; DB 7; Length 248;
Best Local Similarity 76.2%; Pred. No. 2.7e-44;
Matches 93; Conservative 11; Mismatches 12; Indels 6; Gaps 1;

Qy 1 EVOLVQSGAEVKKPQESLRISCKGSDSFTTYWIGVWRQMPGKGLWNGIIPGSDTIY 60
Db 1 QVQLQSAALAKPKQSLKISCKSGFTFTTYWIGVWRQLPGKGLWNGIIPGSDHTTY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCTRGDRGV-----DYWGQGTILTV 114
Db 61 SPSPFEGHVNISVDKSIINTAYLQWSSLKASDTAMYCARHDDDDVLTGYTFESWGQGTMTVT 120

Qy 115 SS 116
Db 121 SS 122

RESULT 5
US-11-054-515-1995
; Sequence 1995, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoespecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1995
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1995

Query Match      79.8%; Score 495.5; DB 7; Length 248;
Best Local Similarity 79.7%; Pred. No. 4.9e-44;
Matches 98; Conservative 6; Mismatches 12; Indels 7; Gaps 2;

Qy 1 EVOLVQSGAEVKKPQESLRISCKGSDSFTTYWIGVWRQMPGKGLWNGIIPGSDTIY 60
Db 1 EVOLVQSGAEVKKPQESLRISCKSGYNFANYWIAVWRQTGKGLQMLGMIIPGSDSETKY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCTR-GDRGV-----DYWGQGTILTV 113
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Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDSAMYICARTSERGYRQWDFNMGQGITLV 120
Qy 114 VSS 116
Db 121 VSS 123

RESULT 6
US-11-054-669-45
; Sequence 45, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-45

Query Match      79.7%; Score 495; DB 7; Length 98;
Best Local Similarity 94.9%; Pred. No. 2.1e-44;
Matches 93; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EVOLVQSGAEVKKPQESLRISCKGSDSFTTYWIGVWRQMPGKGLWNGIIPGSDTIY 60
Db 1 EVOLVQSGAEVKKPQESLRISCKSGYSFTSYWIGVWRQMPGKGLWNGIIPGSDTRY 60

Qy 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCTR 98
Db 61 SPSPQGGVTTISADKSIISTAYLQWSSLKASDTAMYCAR 98

RESULT 7
US-11-084-554-56
; Sequence 56, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Strid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Kotver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-56

Query Match      79.7%; Score 495; DB 7; Length 98;
Best Local Similarity 94.9%; Pred. No. 2.1e-44;
Matches 93; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EVOLVQSGAEVKKPQESLRISCKGSDSFTTYWIGVWRQMPGKGLWNGIIPGSDTIY 60
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Db	Qy	Db
1	EVOLVSGAEVKPGBSLKISCKSGSYFTSYNIQWVRQMPGKLEWIGIILPGSDTRY	60
61	SPSFGQQTIVISADKSIISTAYLOWSSLKASDTAMYYCTR	98
61	SPSFGQQTIVISADKSIISTAYLOWSSLKASDTAMYYCAR	98

RESULT 8
US-11-054-515-1957
; Sequence 1957, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyvS

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/ CURRENT AFFIDAVIT NUMBER: 05/11/03/47315
/
/ CURRENT FILING DATE: 2005-02-10
/
/ PRIOR APPLICATION NUMBER: 60/543,296
/
/ PRIOR FILING DATE: 2004-02-11
/
/ PRIOR APPLICATION NUMBER: 60/580,347
/
/ PRIOR FILING DATE: 2004-06-18
/
/ PRIOR APPLICATION NUMBER: 10/293,418
/
/ PRIOR FILING DATE: 2002-11-14
/
/ PRIOR APPLICATION NUMBER: 60/331,469
/
/ PRIOR FILING DATE: 2001-11-16
/
/ PRIOR APPLICATION NUMBER: 60/340,817
/
/ PRIOR FILING DATE: 2001-12-19
/
/ PRIOR APPLICATION NUMBER: 03/880,748
/
/ PRIOR FILING DATE: 2001-06-15
/
/ PRIOR APPLICATION NUMBER: 60/293,499
/
/ PRIOR FILING DATE: 2001-05-25
/
/ PRIOR APPLICATION NUMBER: 60/277,379
/
/ PRIOR FILING DATE: 2001-03-21
/
/ PRIOR APPLICATION NUMBER: 60/276,248
/
/ PRIOR FILING DATE: 2001-03-16
/
/ PRIOR APPLICATION NUMBER: 60/240,816
/
/ PRIOR FILING DATE: 2000-10-17
/
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/
/ NUMBER OF SEQ ID NOS: 3247
/
/ SEQ ID NO 1957
/
/ LENGTH: 249
/
/ TYPE: PRT
/
/ ORGANISM: Homo sapiens
/
/ US-11-054-515-1957

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; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2103
; LENGTH: 247
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-054-515-2103

```

Query Match	75.8%	Score 470.5	DB 7	Length 247
Best Local Similarity	76.9%	Pred. No. 1.7e-41		
Matches 93	Conservative 8	Mismatches 15	Indels 5	Gaps 2
Qy	1	EVOLVOSGAVKXPGSLRISCKSGSDSFYTWIGVROMPGKLGLEWMGIIYPGDSSTIY	60	
Db	1	EVOLVOSGADVKKPGSLKISCSGSGYTFANYITWVROMPGKLGLEWMGRIDPSDSVTNY	60	
Qy	61	SPSFGQGVITISADKSIStAYLQWSSLKASDTAMYCYCTRG---	DRGV-DYWGQGTLTVTVS	115
Db	61	NPSPFGQGVHTMSVDKSIStAYLQWSSLKASDTAKYCYCARGGVGDSRGVDFPMKGTLTVTVS	120	
Qy	116	\$ 116		
Db	121	\$ 121		

```

RESULT 10
US-11-054-669-124
; Sequence 124, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 124
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-124

```

```
Query Match      72.1%; Score 447.5; DB 7; Length 119;  
Best Local Similarity 74.8%; Pred. No. 1.7e-39;  
Matches 89; Conservative 6; Mismatches 21; Indels 3; Gaps 1;
```

Oy

1 EVLVSGAEVKKPGESLRISCKGSDFTTYWIGWRQMPKGLEWNGIYDGDSTII 60
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

Db 1 EVQLVQSAEAEVKKPGESLRISCKTSGYFTSYNHHVVRQMPGKLEWNGAIYPRSGDTSY 60
Qy 61 SPSPQGVTTISADKSIATYALQWSLKSADTAMYYCTRG---DRGVDYWGQGLTVTVSS 116
Db 61 NPSPQGVTTISADSSSTAYALQWSLKSADTAMYYCTRSYDYDAPFAFWGQGLTVTVSS 119

RESULT 11

US-11-054-515-1514
; Sequence 1514, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1514
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-054-515-1514

Query Match 67.7%; Score 420.5; DB 7; Length 257;
Best Local Similarity 65.1%; Pred. No. 2.1e-36;
Matches 84; Conservative 12; Mismatches 20; Indels 13; Gaps 1;

Qy 1 EVQLVQSAEAEVKKPGESLRISCKGSDSFTTYWIGWVRQMPGKLEWNGIIPGSDTIY 60
Db 1 EVQLVQSAEAEVKKPGESLRISCKGSGYFTDYWISWVRQMPGKLEWNGRIDPSYDDY 60
Qy 61 SPSPQGVTTISADKSIATYALQWSLKSADTAMYYCTR-----GDRGVDYWG 107
Db 61 SPSPKGRVTIISDESNAAYLWDSLQASDSTAYTYCARLKAPYDLYLTKYHLPKWFDTWG 120
Qy 108 QGTLTVTVSS 116
Db 121 QGTLTVTVSS 129

RESULT 12

US-11-096-074-58
; Sequence 58, Application US/11096074
; Publication No. US20050260193A1
; GENERAL INFORMATION:
; APPLICANT: LIEBERBURG, IVAN
; TITLE OF INVENTION: STEROID SPARING AGENTS AND METHODS OF USING SAME
; FILE REFERENCE: 034008-112
; CURRENT APPLICATION NUMBER: US/11/096,074
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/558,120

; PRIOR FILING DATE: 2004-04-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 58
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-074-58

Query Match 65.8%; Score 408.5; DB 7; Length 125;
Best Local Similarity 64.0%; Pred. No. 1.7e-35;
Matches 80; Conservative 16; Mismatches 20; Indels 9; Gaps 2;

Qy 1 EVQLVQSAEAEVKKPGESLRISCKGSDSFTTYWIGWVRQMPGKLEWNGIIPGSDTIY 60
Db 1 QVQLVQSAEAEVKKPGASVKVSCKASGYFTTSYALSWVRQAPGQGLWNGWIPNGGDTNY 60
Qy 61 SPSPQGVTTISADKSIATYALQWSLKSADTAMYYCTR-----GDRG-----VDYWGQGL 111
Db 61 AQKFGKRVTTTADTSTSTAYMELSLRSEDATVYTCARAPGYSGGCVRYDFDYWGQGL 120
Qy 112 VTVSS 116
Db 121 VTVSS 125

RESULT 13

US-11-108-135-24
; Sequence 24, Application US/11108135
; Publication No. US20050260213A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; APPLICANT: Tuailon, Nadine
; APPLICANT: Bonvini, Ezio
; APPLICANT: Stavenhagen, Jeffrey
; APPLICANT: Rankin, Christopher
; TITLE OF INVENTION: FC-gamma-RIIB-specific antibodies and methods of use thereof
; FILE REFERENCE: 11183-014-999
; CURRENT APPLICATION NUMBER: US/11/108,135
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/562,804
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/582,044
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/582,045
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/654,713
; PRIOR FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain variable region
US-11-108-135-24

Query Match 64.3%; Score 399.5; DB 7; Length 121;
Best Local Similarity 62.0%; Pred. No. 1.3e-34;
Matches 75; Conservative 19; Mismatches 22; Indels 5; Gaps 2;

Qy 1 EVQLVQSAEAEVKKPGESLRISCKGSDSFTTYWIGWVRQMPGKLEWNGIIPGSDTIY 60
Db 1 QVQLVQSAEAEVKKPGASVKVSCKASGYFTTYWVVRQAPGQGLWNGWIPDPSITPNY 60
Qy 61 SPSPQGVTTISADKSIATYALQWSLKSADTAMYYCTR-GD---RGVDYWGQGLTVTVS 115
Db 61 NKKFGKRVTTTDTSTSTAYMELSLRSDDTAVYTCARNGSDSYSGMDYWGQGLTVTVS 120
Qy 116 S 116

